GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 3, 2004, 04:34:02 ; Search time 1019.42 Seconds
(without alignments)
1025.182 Million cell updates/sec

Title: US-09-801-371A-2
Perfect score: 43
Sequence: 1 tcaaactggggcctccagaa.....actggggcctacagctttga 43

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	100.0	248	14	T29839	T29839 EST97164 Hu
2	43	100.0	474	13	BX118951	BX118951 BX118951
c 3	43	100.0	630	14	CB528492	CB528492 UI-H-FT2-
c 4	43	100.0	645	14	CD370363	CD370363 UI-H-FT1-
c 5	43	100.0	684	14	CA307429	CA307429 UI-H-FT1-
c 6	43	100.0	688	14	CD367676	CD367676 UI-H-FT1-
c 7	43	100.0	696	14	CA307225	CA307225 UI-H-FT1-
c 8	43	100.0	699	14	CD364761	CD364761 UI-H-FT2-
c 9	43	100.0	703	14	CD368142	CD368142 UI-H-FT1-
c 10	43	100.0	713	14	CA308256	CA308256 UI-H-FT1-
c 11	43	100.0	719	14	CB528694	CB528694 UI-H-FT2-
c 12	43	100.0	722	12	BQ007008	BQ007008 UI-H-EI1-
c 13	43	100.0	722	14	CA307062	CA307062 UI-H-FT1-
c 14	43	100.0	722	14	CD364988	CD364988 UI-H-FT2-
c 15	43	100.0	723	14	CA308777	CA308777 UI-H-FT1-
c 16	43	100.0	723	14	CD368116	CD368116 UI-H-FT1-
c 17	43	100.0	724	14	CA309711	CA309711 UI-H-FT1-
c 18	43	100.0	726	14	CA310368	CA310368 UI-H-FT1-
c 19	43	100.0	726	14	CD368929	CD368929 UI-H-FT1-
c 20	43	100.0	742	14	CA309509	CA309509 UI-H-FT1-
c 21	43	100.0	744	14	CD366187	CD366187 UI-H-FT1-
c 22	43	100.0	748	14	CA306559	CA306559 UI-H-FT1-
c 23	43	100.0	1201	9	AL543083	AL543083 AL543083
c 24	42	97.7	693	14	CD367625	CD367625 UI-H-FT1-
c 25	41.4	96.3	672	14	CD367664	CD367664 UI-H-FT1-
c 26	41.4	96.3	713	14	CA309664	CA309664 UI-H-FT1-
c 27	41.4	96.3	718	14	CD367794	CD367794 UI-H-FT1-
c 28	35.2	81.9	581	9	AI242177	AI242177 qh81g08.x
c 29	33.6	78.1	564	9	AA699697	AA699697 zi78f12.s
c 30	28	65.1	561	10	BG232086	BG232086 naf32e06.
c 31	25	58.1	1011	9	AL575811	AL575811 AL575811
c 32	24.8	57.7	431	28	AQ459761	AQ459761 HS_5125_A
c 33	24.6	57.2	608	14	CB426950	CB426950 602494 MA
34	24	55.8	594	14	N26123	N26123 yx90h08.s1
35	23.8	55.3	163	10	BF737938	BF737938 CM2-KT003
36	23.8	55.3	363	13	BY014887	BY014887 BY014887
37	23.6	54.9	172	10	BF855413	BF855413 RC4-FN020
38	23.4	54.4	434	14	CB759234	CB759234 AMGNNUC:N
39	23.4	54.4	492	13	BY243201	BY243201 BY243201
40	23.4	54.4	763	13	BQ445871	BQ445871 UI-H-EU1-
c 41	23.4	54.4	2686	11	AK077502	AK077502 Mus muscu
c 42	23.2	54.0	1025	13	BQ229625	BQ229625 AGENCOURT
c 43	23.2	54.0	1057	12	BM550588	BM550588 AGENCOURT
44	23	53.5	563	9	AA436782	AA436782 zv70g11.r
45	23	53.5	641	28	BZ158885	BZ158885 CH230-387

ALIGNMENTS

RESULT 1
T29839
LOCUS T29839 248 bp mRNA linear EST 06-SEP-1995
DEFINITION EST97164 Human Testis Homo sapiens cDNA 5' end similar to tumor *necrosis factor, alpha* (HT:1190), mRNA sequence.
ACCESSION T29839
VERSION T29839.1 GI:611937
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 248)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult ,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White ,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald ,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., HinkleJr,P.S., Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei

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           ,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon
           ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
           Venter,J.C.
  TITLE    Initial Assessment of Human Gene Diversity and Expression Patterns
           Based Upon 83 Million Basepairs of cDNA Sequence
  JOURNAL  Nature 377, 3-174 (1995)
  MEDLINE  96026280
   PUBMED  7566098
COMMENT    Contact: Venter, JC
           The Institute for Genomic Research
           932 Clopper Rd, Gaithersburg, MD 20878
           Tel: 3018699056
           Fax: 3018699423
           Email: tdbinfo@tdb.tigr.org
           For clone availability, additional sequence and expression
           information related to this EST, please contact the TIGR Database
           (tdbinfo@tdb.tigr.org)
           Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .248
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="ATCC (inhost):107667"
                     /db_xref="taxon:9606"
                     /clone_lib="Human Testis"
                     /note="Organ: testis"
BASE COUNT       63 a     65 c     60 g     57 t      3 others
ORIGIN

  Query Match             100.0%;  Score 43;  DB 14;  Length 248;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-05;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db         62 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 104


RESULT 2
BX118951
LOCUS       BX118951                 474 bp    mRNA    linear   EST 10-FEB-2003
DEFINITION  BX118951 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
           IMAGp998L124300 ; IMAGE:1693595, mRNA sequence.
ACCESSION   BX118951
VERSION     BX118951.1  GI:27882696
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 474)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
           Radelof,U., Schneider,D. and Korn,B.
  TITLE     Human UnigeneSet - RZPD3
  JOURNAL   Unpublished
COMMENT    Contact: Ina Rolfs
           RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
           Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
           RZPD; IMAGp998L124300.
           RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
           Human UnigeneSet - RZPD3 (RZPDLIB No.972)
           http://www.rzpd.de/CloneCards/cgi-
           bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
           RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
           Heubnerweg 6, D-14059 Berlin, Germany
           Tel: +49 30 32639 101
           Fax: +49 30 32639 111
           www.rzpd.de
           This clone is available royalty-free from RZPD;
           contact RZPD (clone@rzpd.de) for further information. Seq primer:
           M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .474
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGp998L124300 ; IMAGE:1693595"
                     /sex="unknown"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares_fetal_heart_NbHH19W"
                     /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by
                     M.Fatima Bonaldo. This library was constructed from the
                     same fetus as the fetal lung library, Soares fetal lung
                     NbHL19W."
BASE COUNT      112 a    118 c    113 g    131 t
ORIGIN

  Query Match             100.0%;  Score 43;  DB 13;  Length 474;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db         69 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 111


RESULT 3
CB528492/c
LOCUS       CB528492                 630 bp    mRNA    linear   EST 16-MAY-2003
DEFINITION  UI-H-FT2-bjd-e-20-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
           UI-H-FT2-bjd-e-20-0-UI 3', mRNA sequence.
ACCESSION   CB528492
VERSION     CB528492.1  GI:29388228
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 630)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
  JOURNAL   Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Dr. Gary W. Hunninghake, U of I
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
           http://genome.uiowa.edu/distribution/cgap.html
            The following repetitive elements were found in this cDNA
           sequence: 1-29, >AT_rich#Low_complexity (matched compliment)
           205-279, >(TAAA)n#Simple_repeat
           Seq primer: M13 FORWARD
           POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .630
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT2-bjd-e-20-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT2"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
```

modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FT2 is a subtracted cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
subtracted according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. The tissue was provided by Dr.
Gary W. Hunninghake of the University of Iowa.
TAG_LIB=UI-H-FT2
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"

BASE COUNT 180 a 137 c 139 g 174 t
ORIGIN

Query Match 100.0%; Score 43; DB 14; Length 630;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
||||||||||||||||||||||||||||||||||||||||||||
Db 499 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 457

RESULT 4
CD370363/c
LOCUS CD370363 645 bp mRNA linear EST 29-MAY-2003
DEFINITION UI-H-FT1-bkb-n-03-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
UI-H-FT1-bkb-n-03-0-UI 3', mRNA sequence.
ACCESSION CD370363
VERSION CD370363.1 GI:31154453
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 645)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 294-368, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .645
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bkb-n-03-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FT1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG_LIB=UI-H-FT1
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"

BASE COUNT 191 a 145 c 144 g 165 t
ORIGIN

Query Match 100.0%; Score 43; DB 14; Length 645;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
||||||||||||||||||||||||||||||||||||||||||||
Db 588 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 546

RESULT 5
CA307429/c
LOCUS CA307429 684 bp mRNA linear EST 01-NOV-2002
DEFINITION UI-H-FT1-bic-i-01-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
UI-H-FT1-bic-i-01-0-UI 3', mRNA sequence.
ACCESSION CA307429
VERSION CA307429.1 GI:24470483
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 684)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .684
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bic-i-01-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FT1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.

```
                     Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT1
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT       197 a    150 c    158 g    177 t      2 others
ORIGIN

  Query Match             100.0%;  Score 43;  DB 14;  Length 684;
  Best Local Similarity   100.0%;  Pred. No. 0.00012;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        591 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 549


RESULT 6
CD367676/c
LOCUS       CD367676                688 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  UI-H-FT1-bjr-l-14-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bjr-l-14-0-UI 3', mRNA sequence.
ACCESSION   CD367676
VERSION     CD367676.1  GI:31151766
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 688)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 69-143, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .688
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bjr-l-14-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT1
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT       176 a    148 c    181 g    183 t
ORIGIN

  Query Match             100.0%;  Score 43;  DB 14;  Length 688;
  Best Local Similarity   100.0%;  Pred. No. 0.00012;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        363 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 321


RESULT 7
CA307225/c
LOCUS       CA307225                696 bp    mRNA    linear   EST 01-NOV-2002
DEFINITION  UI-H-FT1-bhu-n-04-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bhu-n-04-0-UI 3', mRNA sequence.
ACCESSION   CA307225
VERSION     CA307225.1  GI:24470279
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 696)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 296-370, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .696
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bhu-n-04-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT1
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT       198 a    155 c    160 g    181 t      2 others
ORIGIN
```

```
  Query Match             100.0%;  Score 43;  DB 14;  Length 696;
  Best Local Similarity   100.0%;  Pred. No. 0.00012;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        590 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 548


RESULT 8
CD364761/c
LOCUS       CD364761                699 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  UI-H-FT2-bjm-j-11-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
            UI-H-FT2-bjm-j-11-0-UI 3', mRNA sequence.
ACCESSION   CD364761
VERSION     CD364761.1  GI:31148851
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 699)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 296-370, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .699
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT2-bjm-j-11-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT2"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT2 is a subtracted cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     subtracted according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. The tissue was provided by Dr.
                     Gary W. Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT2
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      200 a    157 c    160 g    182 t
ORIGIN

  Query Match             100.0%;  Score 43;  DB 14;  Length 699;
  Best Local Similarity   100.0%;  Pred. No. 0.00012;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        590 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 548


RESULT 9
CD368142/c
LOCUS       CD368142                703 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  UI-H-FT1-bjv-e-20-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bjv-e-20-0-UI 3', mRNA sequence.
ACCESSION   CD368142
VERSION     CD368142.1  GI:31152232
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 703)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 298-372, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .703
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bjv-e-20-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT1
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      197 a    158 c    161 g    185 t      2 others
ORIGIN

  Query Match             100.0%;  Score 43;  DB 14;  Length 703;
  Best Local Similarity   100.0%;  Pred. No. 0.00012;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        592 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 550


RESULT 10
CA308256/c
LOCUS       CA308256                713 bp    mRNA    linear   EST 01-NOV-2002
DEFINITION  UI-H-FT1-bhy-e-14-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
```

```
          UI-H-FT1-bhy-e-14-0-UI 3', mRNA sequence.
ACCESSION CA308256
VERSION   CA308256.1  GI:24471310
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
  ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1  (bases 1 to 713)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
  JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Dr. Gary W. Hunninghake, U of I
           cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
           cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
           DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
           Clone Distribution: Clone distribution information can be obtained
          from Dr. M. Bento Soares, bento-soares@uiowa.edu
           The following repetitive elements were found in this cDNA
          sequence: 296-370, >(TAAA)n#Simple_repeat
          Seq primer: M13 FORWARD
          POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .713
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bhy-e-14-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT1
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      203 a    164 c    161 g    184 t      1 others
ORIGIN

  Query Match             100.0%;  Score 43;  DB 14;  Length 713;
  Best Local Similarity   100.0%;  Pred. No. 0.00012;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        590 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 548


RESULT 11
CB528694/c
LOCUS       CB528694                719 bp    mRNA    linear   EST 16-MAY-2003
DEFINITION  UI-H-FT2-bjd-l-22-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
          UI-H-FT2-bjd-l-22-0-UI 3', mRNA sequence.
ACCESSION   CB528694
VERSION     CB528694.1  GI:29388630
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1  (bases 1 to 719)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
  JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Dr. Gary W. Hunninghake, U of I
           cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
           cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
           DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
           Clone Distribution: Distribution information can be found at
          http://genome.uiowa.edu/distribution/cgap.html
           The following repetitive elements were found in this cDNA
          sequence: 294-368, >(TAAA)n#Simple_repeat
          Seq primer: M13 FORWARD
          POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .719
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT2-bjd-l-22-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT2"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT2 is a subtracted cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     subtracted according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. The tissue was provided by Dr.
                     Gary W. Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT2
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      203 a    163 c    163 g    188 t      2 others
ORIGIN

  Query Match             100.0%;  Score 43;  DB 14;  Length 719;
  Best Local Similarity   100.0%;  Pred. No. 0.00012;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        588 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 546


RESULT 12
BQ007008/c
LOCUS       BQ007008                722 bp    mRNA    linear   EST 26-MAR-2002
DEFINITION  UI-H-EI1-azb-j-22-0-UI.s1 NCI_CGAP_EI1 Homo sapiens cDNA clone
          IMAGE:5846517 3', mRNA sequence.
ACCESSION   BQ007008
VERSION     BQ007008.1  GI:19731908
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1  (bases 1 to 722)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
  JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
```

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5846517"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_EI1"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_EI1 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACACTTGCAC.
TAG_LIB=UI-H-EI1
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTTGCAC"

BASE COUNT 204 a 162 c 164 g 190 t 2 others
ORIGIN

Query Match 100.0%; Score 43; DB 12; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
||||||||||||||||||||||||||||||||||||||||||||
Db 591 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 549

RESULT 13
CA307062/c
LOCUS CA307062 722 bp mRNA linear EST 01-NOV-2002
DEFINITION UI-H-FT1-bhu-o-04-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone UI-H-FT1-bhu-o-04-0-UI 3', mRNA sequence.
ACCESSION CA307062
VERSION CA307062.1 GI:24470116
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 722)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 295-369, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhu-o-04-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_LIB=UI-H-FT1
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"

BASE COUNT 203 a 165 c 163 g 189 t 2 others
ORIGIN

Query Match 100.0%; Score 43; DB 14; Length 722;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
||||||||||||||||||||||||||||||||||||||||||||
Db 589 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 547

RESULT 14
CD364988/c
LOCUS CD364988 722 bp mRNA linear EST 29-MAY-2003
DEFINITION UI-H-FT2-bjn-c-04-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone UI-H-FT2-bjn-c-04-0-UI 3', mRNA sequence.
ACCESSION CD364988
VERSION CD364988.1 GI:31149078
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 722)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA

```
            sequence: 297-371, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .722
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="UI-H-FT2-bjn-c-04-0-UI"
                      /tissue_type="Aveolar Macrophage"
                      /dev_stage="Adult"
                      /lab_host="DH10B (Life Technologies)"
                      /clone_lib="NCI_CGAP_FT2"
                      /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                      modified polylinker; Site_1: EcoR I; Site_2: Not I;
                      NCI_CGAP_FT2 is a subtracted cDNA library constructed from
                      a pool of 81 RNA samples from Alveolar Macrophages
                      challenged with different treatments. The library was
                      subtracted according to Bonaldo, Lennon and Soares, Genome
                      Research, 6:791-806, 1996. The tissue was provided by Dr.
                      Gary W. Hunninghake of the University of Iowa.
                      TAG_LIB=UI-H-FT2
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                      TAG_SEQ=GGCCATGCCG"
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Db        591 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 549


RESULT 15
CA308777/c
LOCUS       CA308777                723 bp    mRNA    linear   EST 01-NOV-2002
DEFINITION  UI-H-FT1-bhy-b-23-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bhy-b-23-0-UI 3', mRNA sequence.
ACCESSION   CA308777
VERSION     CA308777.1  GI:24471831
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 723)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 297-371, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
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                      /tissue_type="Aveolar Macrophage"
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                      /lab_host="DH10B (Life Technologies)"
                      /clone_lib="NCI_CGAP_FT1"
                      /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                      modified polylinker; Site_1: EcoR I; Site_2: Not I;
                      NCI_CGAP_FT1 is a normalized cDNA library constructed from
                      a pool of 81 RNA samples from Alveolar Macrophages
                      challenged with different treatments. The library was
                      normalized according to Bonaldo, Lennon and Soares, Genome
                      Research, 6:791-806, 1996. First strand cDNA synthesis was
                      primed with an oligo-dT primer containing a Not I site.
                      Double stranded cDNA was ligated to an EcoR I adaptor,
                      digested with Not I, and cloned directionally into
                      pT7T3-Pac vector. The oligonucleotide used to prime the
                      synthesis of first-strand cDNA contains a library tag
                      sequence that is located between the Not I site and the
                      (dT)18 tail. The sequence tag for this library is
                      GGCCATGCCG. The tissue was provided by Dr. Gary W.
                      Hunninghake of the University of Iowa.
                      TAG_LIB=UI-H-FT1
                      TAG_TISSUE=Human Lung Aveolar Macrophage
                      TAG_SEQ=GGCCATGCCG"
BASE COUNT      203 a    164 c    164 g    191 t      1 others
ORIGIN

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  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Job time : 1022.42 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 3, 2004, 05:14:03 ; Search time 764.932 Seconds
(without alignments)
207.072 Million cell updates/sec

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Perfect score: 43
Sequence: 1 tcaaactggggcctccagaa.....actggggcctacagctttga 43

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	43	100.0	43	10	US-09-801-371A-6	Sequence 6, Appli
3	43	100.0	50	10	US-09-801-371A-8	Sequence 8, Appli
4	43	100.0	81	10	US-09-801-371A-7	Sequence 7, Appli
5	43	100.0	104	10	US-09-801-371A-1	Sequence 1, Appli
c 6	43	100.0	104	10	US-09-801-371A-5	Sequence 5, Appli
7	43	100.0	1279	13	US-10-247-671-120	Sequence 120, App
8	43	100.0	1643	13	US-10-310-793-9	Sequence 9, Appli
9	43	100.0	1643	15	US-10-272-411-4	Sequence 4, Appli
10	43	100.0	1643	15	US-10-218-547-3	Sequence 3, Appli
11	43	100.0	1643	15	US-10-272-328A-4	Sequence 4, Appli
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13	43	100.0	3634	11	US-09-824-322B-1	Sequence 1, Appli
14	43	100.0	3634	11	US-09-932-300-34	Sequence 34, Appl
15	43	100.0	3634	13	US-10-191-997-104	Sequence 104, App
16	43	100.0	4830	12	US-10-429-802-33	Sequence 33, Appl
17	43	100.0	4830	12	US-10-430-503-24	Sequence 24, Appl
18	35	81.4	418	10	US-09-796-692-6223	Sequence 6223, Ap
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21	35	81.4	418	15	US-10-040-862-6223	Sequence 6223, Ap
22	30.6	71.2	51	10	US-09-801-371A-10	Sequence 10, Appl
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c 27	22.6	52.6	232	12	US-10-242-535A-46829	Sequence 46829, A
c 28	22.6	52.6	612	13	US-10-027-632-110698	Sequence 110698,
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c 31	22.4	52.1	922	14	US-10-027-632-120081	Sequence 120081,
32	22.2	51.6	27	10	US-09-801-371A-11	Sequence 11, Appl
33	22.2	51.6	3673778	13	US-10-312-841-1	Sequence 1, Appli
34	22	51.2	363	10	US-09-783-590-10563	Sequence 10563, A
35	21.4	49.8	406	10	US-09-560-863-146	Sequence 146, App
c 36	21.4	49.8	614	13	US-10-027-632-279282	Sequence 279282,
c 37	21.4	49.8	614	14	US-10-027-632-279282	Sequence 279282,
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c 39	21.4	49.8	1274	10	US-09-981-876-72	Sequence 72, Appl
c 40	21.4	49.8	1274	11	US-09-148-545-72	Sequence 72, Appl
c 41	21.4	49.8	1296	10	US-09-981-876-126	Sequence 126, App
c 42	21.4	49.8	1296	11	US-09-148-545-126	Sequence 126, App
c 43	21.4	49.8	1343	10	US-09-925-300-779	Sequence 779, App
c 44	21.4	49.8	3113	11	US-09-764-891-5580	Sequence 5580, Ap
c 45	21.4	49.8	4831	13	US-10-252-157-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-801-371A-2
; Sequence 2, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-2

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Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-801-371A-6/c
; Sequence 6, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:

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;  APPLICANT: Kaempfer, Raymond
;  APPLICANT:  Osman, Farhat
;  APPLICANT:  Jarrous, Nayef
;  APPLICANT:  Ben-Asouli, Yitzhak
;  TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
;  TITLE OF INVENTION:  MANIPULATION OF MRNA SPLICING AND ITS USES
;  FILE REFERENCE: A34084-PCT-USA-A 066031.0147
;  CURRENT APPLICATION NUMBER: US/09/801,371A
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: PCT WO 00/14255
;  PRIOR FILING DATE: 1999-09-06
;  NUMBER OF SEQ ID NOS: 12
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; SEQ ID NO 6
;   LENGTH: 43
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-801-371A-6

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RESULT 3
US-09-801-371A-8
; Sequence 8, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
;  APPLICANT: Kaempfer, Raymond
;  APPLICANT:  Osman, Farhat
;  APPLICANT:  Jarrous, Nayef
;  APPLICANT:  Ben-Asouli, Yitzhak
;  TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
;  TITLE OF INVENTION:  MANIPULATION OF MRNA SPLICING AND ITS USES
;  FILE REFERENCE: A34084-PCT-USA-A 066031.0147
;  CURRENT APPLICATION NUMBER: US/09/801,371A
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: PCT WO 00/14255
;  PRIOR FILING DATE: 1999-09-06
;  NUMBER OF SEQ ID NOS: 12
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;   LENGTH: 50
;   TYPE: RNA
;   ORGANISM: Homo sapien
US-09-801-371A-8

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RESULT 4
US-09-801-371A-7
; Sequence 7, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
;  APPLICANT: Kaempfer, Raymond
;  APPLICANT:  Osman, Farhat
;  APPLICANT:  Jarrous, Nayef
;  APPLICANT:  Ben-Asouli, Yitzhak
;  TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
;  TITLE OF INVENTION:  MANIPULATION OF MRNA SPLICING AND ITS USES
;  FILE REFERENCE: A34084-PCT-USA-A 066031.0147
;  CURRENT APPLICATION NUMBER: US/09/801,371A
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: PCT WO 00/14255
;  PRIOR FILING DATE: 1999-09-06
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US-09-801-371A-7

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; Sequence 1, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
;  APPLICANT: Kaempfer, Raymond
;  APPLICANT:  Osman, Farhat
;  APPLICANT:  Jarrous, Nayef
;  APPLICANT:  Ben-Asouli, Yitzhak
;  TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
;  TITLE OF INVENTION:  MANIPULATION OF MRNA SPLICING AND ITS USES
;  FILE REFERENCE: A34084-PCT-USA-A 066031.0147
;  CURRENT APPLICATION NUMBER: US/09/801,371A
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: PCT WO 00/14255
;  PRIOR FILING DATE: 1999-09-06
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;   ORGANISM: Homo sapiens
US-09-801-371A-1

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RESULT 6
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; Sequence 5, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
;  APPLICANT: Kaempfer, Raymond
;  APPLICANT:  Osman, Farhat
;  APPLICANT:  Jarrous, Nayef
;  APPLICANT:  Ben-Asouli, Yitzhak
;  TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
;  TITLE OF INVENTION:  MANIPULATION OF MRNA SPLICING AND ITS USES
;  FILE REFERENCE: A34084-PCT-USA-A 066031.0147
;  CURRENT APPLICATION NUMBER: US/09/801,371A
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: PCT WO 00/14255
;  PRIOR FILING DATE: 1999-09-06
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
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;   ORGANISM: Homo sapien
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RESULT 7
US-10-247-671-120
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; Publication No. US20030194721A1
; GENERAL INFORMATION:
;  APPLICANT: Mikita, Thomas
;  APPLICANT:  Shiffman, Dov
;  APPLICANT:  Porter, Gordon, J.
;  APPLICANT:  Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
;  FILE REFERENCE: PA-0050 US
;  CURRENT APPLICATION NUMBER: US/10/247,671
;  CURRENT FILING DATE:  2002-09-18
;  PRIOR APPLICATION NUMBER: 60/323,784
;  PRIOR FILING DATE: 2001-09-19
;  NUMBER OF SEQ ID NOS: 186
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; SEQ ID NO 120
;   LENGTH: 1279
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;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030194721A1 561301CB1
US-10-247-671-120

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RESULT 8
US-10-310-793-9
; Sequence 9, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
;  APPLICANT: Yu, Guo-Liang
;  APPLICANT:  Ni, Jian
;  APPLICANT:  Rosen, Craig A
;  APPLICANT:  Zhang, Jun
;  APPLICANT:  Wei, Ping
;  TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
;  TITLE OF INVENTION:  Relating To Human Tumor Necrosis Factor-Gamma Beta
;  FILE REFERENCE: PF573
;  CURRENT APPLICATION NUMBER: US/10/310,793
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: 60/336,695
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: 10/226,294
;  PRIOR FILING DATE: 2002-08-23
;  PRIOR APPLICATION NUMBER: 60/314,381
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: 09/899,059
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/278,449
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: 60/216,879
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: 09/559,290
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/180,908
;  PRIOR FILING DATE: 2000-02-08
;  PRIOR APPLICATION NUMBER: 60/134,067
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/132,227
;  PRIOR FILING DATE: 1999-05-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 71
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;   ORGANISM: human
US-10-310-793-9

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Db       1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116


RESULT 9
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; Sequence 4, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
;  APPLICANT: Barnes Jewish Hospital
;  APPLICANT:  Lam, Jonathan
;  APPLICANT:  Ross, F. Patrick
;  APPLICANT:  Teitelbaum, Steven
;  TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
;  FILE REFERENCE: 60019620-0202
;  CURRENT APPLICATION NUMBER: US/10/272,411
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/329,393
;  PRIOR FILING DATE: 2001-10-15
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1643
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/ X01394.1
;   DATABASE ENTRY DATE: 1995-03-21
;   RELEVANT RESIDUES: (1)..(1643)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
;   DATABASE ENTRY DATE: 2002-05-01
;   RELEVANT RESIDUES: (1)..(1643)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/ M35592.1
;   DATABASE ENTRY DATE: 1993-04-27
;   RELEVANT RESIDUES: (1)..(1643)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
;   DATABASE ENTRY DATE: 2002-08-01
;   RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4

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  Best Local Similarity   100.0%;  Pred. No. 5.7e-08;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db       1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116


RESULT 10
US-10-218-547-3
; Sequence 3, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
;  TITLE OF INVENTION:  Human Endokine Alpha
;  FILE REFERENCE: PF561
;  CURRENT APPLICATION NUMBER: US/10/218,547
;  CURRENT FILING DATE:  2002-08-15
;  PRIOR APPLICATION NUMBER: 60/312,542
;  PRIOR FILING DATE: 2001-08-16
;  PRIOR APPLICATION NUMBER: 60/330,761
;  PRIOR FILING DATE: 2001-10-30
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 1643
;   TYPE: DNA
;   ORGANISM: human
US-10-218-547-3

  Query Match             100.0%;  Score 43;  DB 15;  Length 1643;
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  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116


RESULT 11
US-10-272-328A-4
; Sequence 4, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
;  APPLICANT: Barnes Jewish Hospital
;  APPLICANT:  Lam, Jonathan
;  APPLICANT:  Ross, F. Patrick
;  APPLICANT:  Teitelbaum, Steven
;  TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
;  FILE REFERENCE: 60019620-0206
;  CURRENT APPLICATION NUMBER: US/10/272,328A
;  CURRENT FILING DATE:  2003-01-24
;  PRIOR APPLICATION NUMBER: 60/329,393
;  PRIOR FILING DATE: 2001-10-15
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1643
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-272-328A-4

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Db       1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116


RESULT 12
US-10-247-671-68
; Sequence 68, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
;  APPLICANT: Mikita, Thomas
;  APPLICANT:  Shiffman, Dov
;  APPLICANT:  Porter, Gordon, J.
;  APPLICANT:  Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
;  FILE REFERENCE: PA-0050 US
;  CURRENT APPLICATION NUMBER: US/10/247,671
;  CURRENT FILING DATE:  2002-09-18
;  PRIOR APPLICATION NUMBER: 60/323,784
;  PRIOR FILING DATE: 2001-09-19
;  NUMBER OF SEQ ID NOS: 186
;  SOFTWARE: PERL Program
; SEQ ID NO 68
;   LENGTH: 1666
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030194721A1 223092.1
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 1347, 1358
;   OTHER INFORMATION: a, t, c, g, or other
US-10-247-671-68

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Db       1089 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1131


RESULT 13
US-09-824-322B-1
; Sequence 1, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Butler, Madeline M.
;  APPLICANT:  Shanahan, William R.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-AL
;  TITLE OF INVENTION:  ALPHA) EXPRESSION
;  FILE REFERENCE: ISPH-0501
;  CURRENT APPLICATION NUMBER: US/09/824,322B
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: US 09/313,932
;  PRIOR FILING DATE: 1999-05-18
;  PRIOR APPLICATION NUMBER: US 09/166,186
;  PRIOR FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 1
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
;   NAME/KEY: exon
;   LOCATION: (615)..(981)
;   NAME/KEY: intron
;   LOCATION: (982)..(1588)
;   NAME/KEY: exon
;   LOCATION: (1589)..(1634)
;   NAME/KEY: intron
;   LOCATION: (1635)..(1821)
;   NAME/KEY: exon
;   LOCATION: (1822)..(1869)
;   NAME/KEY: intron
;   LOCATION: (1870)..(2070)
;   NAME/KEY: exon
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;   LOCATION: (2171)..(3381)
;  PUBLICATION INFORMATION:
;   AUTHORS: Nedwin, G.E.
;   AUTHORS: Naylor, S.L.
;   AUTHORS: Sakaguchi, A.Y.
;   AUTHORS: Smith, D.
;   AUTHORS: Jarrett-Nedwin, J.
;   AUTHORS: Pennica, D.
;   AUTHORS: Goeddel, D.V.
;   AUTHORS: Gray, P.W.
;   TITLE: Human lymphotoxin and tumor necrosis factor genes: structure, homology and
;   TITLE: chromosomal localization
;   JOURNAL: Nucleic Acids Res.
;   VOLUME: 13
;   ISSUE: 17
;   PAGES: 6361-6373
;   DATE: 1985-09-11
;   DATABASE ACCESSION NUMBER: X02910 Genbank
;   DATABASE ENTRY DATE: 1997-02-17
US-09-824-322B-1

  Query Match             100.0%;  Score 43;  DB 11;  Length 3634;
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  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 14
US-09-932-300-34
; Sequence 34, Application US/09932300
; Publication No. US20030032788A1
; GENERAL INFORMATION:
;  APPLICANT: GARVER, Eric
;  APPLICANT:  TU, Guang-Chou
;  APPLICANT:  ISRAEL, Yedy
;  TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION
;  FILE REFERENCE: 9855-3U2
;  CURRENT APPLICATION NUMBER: US/09/932,300
;  CURRENT FILING DATE:  2001-08-20
;  PRIOR APPLICATION NUMBER: US 60/051,705
;  PRIOR FILING DATE: 1997-07-03
;  PRIOR APPLICATION NUMBER: US 09/109,663
;  PRIOR FILING DATE: 1998-07-02
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-932-300-34

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  Best Local Similarity   100.0%;  Pred. No. 5.8e-08;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||||||||||||||||||||||
Db       2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854


RESULT 15
US-10-191-997-104
; Sequence 104, Application US/10191997
; Publication No. US20030207834A1
; GENERAL INFORMATION:
;  APPLICANT: Oligos Etc., Inc.
;  APPLICANT:  DALE, Roderic M. K.
;  APPLICANT:  ARROW, Amy
;  APPLICANT:  THOMPSON, Terry
;  TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their
;  FILE REFERENCE: 54800-5019
;  CURRENT APPLICATION NUMBER: US/10/191,997
;  CURRENT FILING DATE:  2002-07-10
;  PRIOR APPLICATION NUMBER: US 60/303,820
;  PRIOR FILING DATE: 2001-07-10
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: X02910
US-10-191-997-104

  Query Match             100.0%;  Score 43;  DB 13;  Length 3634;
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Perfect score: 43
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	100.0	787	4	US-09-032-297A-13	Sequence 13, Appl
2	43	100.0	787	4	US-09-229-151C-7	Sequence 7, Appli
3	43	100.0	1643	3	US-08-880-342-36	Sequence 36, Appl
4	43	100.0	1643	4	US-09-505-250-4	Sequence 4, Appli
5	43	100.0	2270	4	US-09-229-151C-13	Sequence 13, Appl
6	43	100.0	2570	4	US-09-229-151C-14	Sequence 14, Appl
7	43	100.0	3634	3	US-09-166-186-1	Sequence 1, Appli
8	43	100.0	3634	3	US-09-313-932-1	Sequence 1, Appli
9	43	100.0	3634	3	US-09-109-663-34	Sequence 34, Appl
10	21.4	49.8	24707	4	US-09-740-027-3	Sequence 3, Appli
11	21	48.8	771	5	PCT-US95-12987-1	Sequence 1, Appli
12	21	48.8	771	5	PCT-US95-12987-3	Sequence 3, Appli
13	21	48.8	771	5	PCT-US95-12987-5	Sequence 5, Appli
14	20.8	48.4	861	1	US-08-409-731A-1	Sequence 1, Appli
15	20.8	48.4	861	2	US-08-470-298B-1	Sequence 1, Appli
16	20.8	48.4	861	2	US-09-023-073A-1	Sequence 1, Appli
17	20.8	48.4	861	3	US-09-361-737-1	Sequence 1, Appli
18	20.8	48.4	944	2	US-08-820-825-1	Sequence 1, Appli
19	20.8	48.4	944	3	US-09-307-817-1	Sequence 1, Appli
20	20.8	48.4	944	4	US-09-734-036-1	Sequence 1, Appli
21	20.8	48.4	957	3	US-08-899-031-2	Sequence 2, Appli
22	20.8	48.4	65042	4	US-09-784-316-3	Sequence 3, Appli
c 23	20	46.5	20	3	US-09-166-186-32	Sequence 32, Appl
c 24	20	46.5	20	3	US-09-166-186-212	Sequence 212, App
c 25	20	46.5	20	3	US-09-166-186-213	Sequence 213, App
c 26	20	46.5	20	3	US-09-166-186-214	Sequence 214, App
c 27	20	46.5	20	3	US-09-313-932-32	Sequence 32, Appl
c 28	20	46.5	20	3	US-09-313-932-212	Sequence 212, App
c 29	20	46.5	20	3	US-09-313-932-213	Sequence 213, App
c 30	20	46.5	20	3	US-09-313-932-214	Sequence 214, App
c 31	20	46.5	20	3	US-09-313-932-354	Sequence 354, App
c 32	20	46.5	20	3	US-09-313-932-357	Sequence 357, App
c 33	20	46.5	20	3	US-09-313-932-358	Sequence 358, App
c 34	20	46.5	20	3	US-09-313-932-361	Sequence 361, App
c 35	20	46.5	20	3	US-09-313-932-468	Sequence 468, App
c 36	19.8	46.0	3431	4	US-09-632-098-1	Sequence 1, Appli
c 37	19.8	46.0	3468	4	US-09-632-098-3	Sequence 3, Appli
38	19.8	46.0	4695	2	US-08-231-193A-57	Sequence 57, Appl
39	19.8	46.0	4695	2	US-08-486-273A-57	Sequence 57, Appl
40	19.8	46.0	4695	3	US-08-940-086A-57	Sequence 57, Appl
41	19.8	46.0	4695	4	US-08-940-035A-57	Sequence 57, Appl
42	19.8	46.0	4695	4	US-08-935-105A-57	Sequence 57, Appl
43	19.8	46.0	4695	4	US-09-648-797-57	Sequence 57, Appl
44	19.8	46.0	4695	4	US-09-386-123-57	Sequence 57, Appl
c 45	19.4	45.1	298	4	US-09-313-294A-5776	Sequence 5776, Ap

ALIGNMENTS

RESULT 1
US-09-032-297A-13
; Sequence 13, Application US/09032297A
; Patent No. 6525184
; GENERAL INFORMATION:
; APPLICANT: Revati J. Tatake, Steven D. Marlin and
; Randall W. Barton
; TITLE OF INVENTION: Self-Regulated Apoptosis of
; Inflammatory Cells by Gene Therapy
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Boehringer Ingelheim Corporation
; STREET: 900 Ridgebury Road, P.O. Box 368
; CITY: Ridgefield
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06877-0368
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,297A
; FILING DATE: 27-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,266
; FILING DATE: 28-FEB-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert P. Raymond
; REGISTRATION NUMBER: 25089
; REFERENCE/DOCKET NUMBER: 9/121PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-791-6183
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: DNA
; FEATURE:
; NAME/KEY: TNFa 3' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-032-297A-13

Query Match 100.0%; Score 43; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;

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Db        226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268


RESULT 2
US-09-229-151C-7
; Sequence 7, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
;  APPLICANT: Tatake, Revati J.
;  APPLICANT:  Marlin, Steven D.
;  APPLICANT:  Barton, Randall W.
;  TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
;  FILE REFERENCE: 9/137
;  CURRENT APPLICATION NUMBER: US/09/229,151C
;  CURRENT FILING DATE:  1999-01-12
;  PRIOR APPLICATION NUMBER: US 60/076,316
;  PRIOR FILING DATE: 1998-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 2.0
; SEQ ID NO 7
;   LENGTH: 787
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   OTHER INFORMATION: TNF-alpha untranslated region
US-09-229-151C-7

  Query Match            100.0%;  Score 43;  DB 4;  Length 787;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-08;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db        226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268


RESULT 3
US-08-880-342-36
; Sequence 36, Application US/08880342
; Patent No. 6218179
;  GENERAL INFORMATION:
;    APPLICANT:  Webster, Keith A.
;    APPLICANT:  Bishopric, Nanette H.
;    APPLICANT:  Murphy, Brian
;    APPLICANT:  Laderoute, Keith R.
;    APPLICANT:  Green, Christopher J.
;    TITLE OF INVENTION:  Tissue Specific Hypoxia Regulated
;    TITLE OF INVENTION:  Therapeutic Constructs
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/880,342
;      FILING DATE:  23-JUN-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB95/00996
;      FILING DATE:  13-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/365,486
;      FILING DATE:  23-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sholtz, Charles K.
;      REGISTRATION NUMBER:  38,615
;      REFERENCE/DOCKET NUMBER:  8255-0018.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1643 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  TNF cDNA HSTNFR (EMBL Accession
;      INDIVIDUAL ISOLATE:  #X01394)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  153..851
US-08-880-342-36

  Query Match            100.0%;  Score 43;  DB 3;  Length 1643;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-08;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db       1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116


RESULT 4
US-09-505-250-4
; Sequence 4, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
;  APPLICANT:  Rosen, Glenn
;  APPLICANT:  Kao, Peter
;  TITLE OF INVENTION:  Synergistic Anti-Cancer Therapy with
;  TITLE OF INVENTION:  Triptolides and Death Domain Ligands
;  FILE REFERENCE:  SUN-109PRV2
;  CURRENT APPLICATION NUMBER: US/09/505,250A
;  CURRENT FILING DATE:  2000-02-15
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 1643
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (153)...(854)
US-09-505-250-4

  Query Match            100.0%;  Score 43;  DB 4;  Length 1643;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-08;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              ||||||||||||||||||||||||||||||||||||||||||
Db       1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116


RESULT 5
US-09-229-151C-13
; Sequence 13, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
;  APPLICANT: Tatake, Revati J.
```

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;  APPLICANT:  Marlin, Steven D.
;  APPLICANT:  Barton, Randall W.
;  TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
;  FILE REFERENCE: 9/137
;  CURRENT APPLICATION NUMBER: US/09/229,151C
;  CURRENT FILING DATE:  1999-01-12
;  PRIOR APPLICATION NUMBER: US 60/076,316
;  PRIOR FILING DATE: 1998-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 2.0
; SEQ ID NO 13
;   LENGTH: 2270
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   OTHER INFORMATION: chimeric gene : -706TNFpGB3'UTR
US-09-229-151C-13

  Query Match             100.0%;  Score 43;  DB 4;  Length 2270;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-08;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db       1709 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1751


RESULT 6
US-09-229-151C-14
; Sequence 14, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
;  APPLICANT: Tatake, Revati J.
;  APPLICANT:  Marlin, Steven D.
;  APPLICANT:  Barton, Randall W.
;  TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
;  FILE REFERENCE: 9/137
;  CURRENT APPLICATION NUMBER: US/09/229,151C
;  CURRENT FILING DATE:  1999-01-12
;  PRIOR APPLICATION NUMBER: US 60/076,316
;  PRIOR FILING DATE: 1998-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 2.0
; SEQ ID NO 14
;   LENGTH: 2570
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   OTHER INFORMATION: chimeric gene : -1005TNFpGB3'UTR
US-09-229-151C-14

  Query Match             100.0%;  Score 43;  DB 4;  Length 2570;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-08;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db       2009 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2051


RESULT 7
US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda
;  APPLICANT: Bennett, C. Frank
;  APPLICANT: Butler, Madeline M.
;  APPLICANT: Shanahan, William R.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
;  FILE REFERENCE: ISPH-0322
;  CURRENT APPLICATION NUMBER: US/09/166,186A
;  CURRENT FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 1
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (615)..(981)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (982)..(1588)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1589)..(1634)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (1635)..(1821)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1822)..(1869)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (1870)..(2070)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (2171)..(3381)
;   PUBLICATION INFORMATION:
;   AUTHORS: Nedwin, G.E.
;   AUTHORS: Naylor, S.L.
;   AUTHORS: Sakaguchi, A.Y.
;   AUTHORS: Smith, D.
;   AUTHORS: Jarrett-Nedwin, J.
;   AUTHORS: Pennica, D.
;   AUTHORS: Goeddel, D.V.
;   AUTHORS: Gray, P.W.
;   TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,
;   TITLE: homology and chromosomal localization
;   JOURNAL: Nucleic Acids Res.
;   VOLUME: 13
;   ISSUE: 17
;   PAGES: 6361-6373
;   DATE: 1985-09-11
;   DATABASE ACCESSION NUMBER: X02910 Genbank
;   DATABASE ENTRY DATE: 1997-02-17
US-09-166-186-1

  Query Match             100.0%;  Score 43;  DB 3;  Length 3634;
  Best Local Similarity   100.0%;  Pred. No. 2e-08;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db       2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854


RESULT 8
US-09-313-932-1
; Sequence 1, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda
;  APPLICANT: Bennett, C. Frank
;  APPLICANT: Butler, Madeline M.
;  APPLICANT: Shanahan, William R.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
;  TITLE OF INVENTION: EXPRESSION
;  FILE REFERENCE: ISPH-0356
;  CURRENT APPLICATION NUMBER: US/09/313,932A
;  CURRENT FILING DATE: 1999-05-18
;  NUMBER OF SEQ ID NOS: 501
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; SEQ ID NO 1
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (615)..(981)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (982)..(1588)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1589)..(1634)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (1635)..(1821)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1822)..(1869)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (1870)..(2070)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (2171)..(3381)
;  PUBLICATION INFORMATION:
;   AUTHORS: Nedwin, G.E.
;   AUTHORS: Naylor, S.L.
;   AUTHORS: Sakaguchi, A.Y.
;   AUTHORS: Smith, D.
;   AUTHORS: Jarrett-Nedwin, J.
;   AUTHORS: Pennica, D.
;   AUTHORS: Goeddel, D.V.
;   AUTHORS: Gray, P.W.
;   TITLE: Human lymphotoxin and tumor necrosis factor genes:
;   TITLE: structure, homology and chromosomal localization
;   JOURNAL: Nucleic Acids Res.
;   VOLUME: 13
;   ISSUE: 17
;   PAGES: 6361-6373
;   DATE: 1985-09-11
;   DATABASE ACCESSION NUMBER: X02910 Genbank
;   DATABASE ENTRY DATE: 1997-02-17
US-09-313-932-1

  Query Match            100.0%;  Score 43;  DB 3;  Length 3634;
  Best Local Similarity   100.0%;  Pred. No. 2e-08;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db       2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854


RESULT 9
US-09-109-663-34
; Sequence 34, Application US/09109663
; Patent No. 6277981
; GENERAL INFORMATION:
;  APPLICANT: Tu, Guang-Chou
;  APPLICANT: Israel, Yedy
;  TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
;  TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
;  FILE REFERENCE: 9855-3U1
;  CURRENT APPLICATION NUMBER: US/09/109,663
;  CURRENT FILING DATE: 1998-07-03
;  EARLIER APPLICATION NUMBER: 60/051,705
;  EARLIER FILING DATE: 1997-07-03
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: TNF(alpha) cDNA
US-09-109-663-34

  Query Match            100.0%;  Score 43;  DB 3;  Length 3634;
  Best Local Similarity   100.0%;  Pred. No. 2e-08;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db       2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854


RESULT 10
US-09-740-027-3
; Sequence 3, Application US/09740027
; Patent No. 6485939
; GENERAL INFORMATION:
;  APPLICANT: YE, Jane et al
;  TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER COFACTOR
;  TITLE OF INVENTION:  PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER
;  TITLE OF INVENTION:  COFACTOR PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL001052
;  CURRENT APPLICATION NUMBER: US/09/740,027
;  CURRENT FILING DATE:  2000-12-20
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 24707
;   TYPE: DNA
;   ORGANISM: Human
US-09-740-027-3

  Query Match            49.8%;  Score 21.4;  DB 4;  Length 24707;
  Best Local Similarity   80.6%;  Pred. No. 16;
  Matches   25;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGC 31
              ||  |||  | ||||| ||||||||||||||
Db      11941 TCCCACTTTGCCCTCCGGAACTCACTGGGGC 11971


RESULT 11
PCT-US95-12987-1
; Sequence 1, Application PC/TUS9512987
;  GENERAL INFORMATION:
;    APPLICANT:  LAFEMINA, R.
;    APPLICANT:  SARDANA, V.
;    APPLICANT:  VELOSKI, C.
;    TITLE OF INVENTION:  STABLE RECOMBINANT HCMV PROTEASE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROY D. MEREDITH
;      STREET:  P.O. BOX 2000, 126 E. LINCOLN AVE.
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/12987
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MEREDITH, ROY D.
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;      REGISTRATION NUMBER:  30,777
;      REFERENCE/DOCKET NUMBER:  19262 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-4678
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US95-12987-1

  Query Match             48.8%;  Score 21;  DB 5;  Length 771;
  Best Local Similarity   73.0%;  Pred. No. 13;
  Matches   27;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAG 37
              ||| || | ||  |||||| ||||| | |||| || |
Db        539 TCACACAGCGGTTTCCAGACCTCACGGCGGCCGACCG 575


RESULT 12
PCT-US95-12987-3
; Sequence 3, Application PC/TUS9512987
;  GENERAL INFORMATION:
;    APPLICANT:  LAFEMINA, R.
;    APPLICANT:  SARDANA, V.
;    APPLICANT:  VELOSKI, C.
;    TITLE OF INVENTION:  STABLE RECOMBINANT HCMV PROTEASE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROY D. MEREDITH
;      STREET:  P.O. BOX 2000, 126 E. LINCOLN AVE.
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/12987
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MEREDITH, ROY D.
;      REGISTRATION NUMBER:  30,777
;      REFERENCE/DOCKET NUMBER:  19262 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-4678
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US95-12987-3

  Query Match             48.8%;  Score 21;  DB 5;  Length 771;
  Best Local Similarity   73.0%;  Pred. No. 13;
  Matches   27;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAG 37
              ||| || | ||  |||||| ||||| | |||| || |
Db        539 TCACACAGCGGTTTCCAGACCTCACGGCGGCCGACCG 575


RESULT 13
PCT-US95-12987-5
; Sequence 5, Application PC/TUS9512987
;  GENERAL INFORMATION:
;    APPLICANT:  LAFEMINA, R.
;    APPLICANT:  SARDANA, V.
;    APPLICANT:  VELOSKI, C.
;    TITLE OF INVENTION:  STABLE RECOMBINANT HCMV PROTEASE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROY D. MEREDITH
;      STREET:  P.O. BOX 2000, 126 E. LINCOLN AVE.
;      CITY:  RAHWAY
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/12987
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MEREDITH, ROY D.
;      REGISTRATION NUMBER:  30,777
;      REFERENCE/DOCKET NUMBER:  19262 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 594-4678
;      TELEFAX:  (908) 594-4720
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  771 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US95-12987-5

  Query Match             48.8%;  Score 21;  DB 5;  Length 771;
  Best Local Similarity   73.0%;  Pred. No. 13;
  Matches   27;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAG 37
              ||| || | ||  |||||| ||||| | |||| || |
Db        539 TCACACAGCGGTTTCCAGACCTCACGGCGGCCGACCG 575


RESULT 14
US-08-409-731A-1
; Sequence 1, Application US/08409731A
; Patent No. 5658758
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Yu, Guo-Liang
;    APPLICANT:  Gentz, Reiner
;    APPLICANT:  Rosen, Craig A.
;    TITLE OF INVENTION:  CYTOSTATIN I
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HUMAN GENOME SCIENCES, INC.
;      STREET:  9410 KEY WEST AVENUE
;      CITY:  ROCKVILLE
;      STATE:  MD
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/409,731A
;      FILING DATE:  24-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Robert H
;      REGISTRATION NUMBER:  30,446
;      REFERENCE/DOCKET NUMBER:  PF175
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-309-8504
;      TELEFAX:  301-309-8512
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  861 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  94..414
US-08-409-731A-1

  Query Match             48.4%;  Score 20.8;  DB 1;  Length 861;
  Best Local Similarity   78.1%;  Pred. No. 16;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         11 GCCTCCAGAACTCACTGGGGCCTACAGCTTTG 42
              ||||||  | ||||||||   |||| ||||||
Db         96 GCCTCCCAACCTCACTGGCTACTACCGCTTTG 127


RESULT 15
US-08-470-298B-1
; Sequence 1, Application US/08470298B
; Patent No. 5844081
;  GENERAL INFORMATION:
;    APPLICANT:  NI, JIAN
;    APPLICANT:  GENTZ, REINER
;    APPLICANT:  YU, GUO-LIANG
;    APPLICANT:  ROSEN, CRAIG A.
;    TITLE OF INVENTION:  CYTOSTATIN I
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HUMAN GENOME SCIENCES, INC.
;      STREET:  9410 KEY WEST AVENUE
;      CITY:  ROCKVILLE
;      STATE:  MD
;      COUNTRY:  US
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,298B
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BROOKES, ALLAN A.
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PF175D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-309-8504
;      TELEFAX:  301-309-8512
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  861 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  94..414
US-08-470-298B-1

  Query Match             48.4%;  Score 20.8;  DB 2;  Length 861;
  Best Local Similarity   78.1%;  Pred. No. 16;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         11 GCCTCCAGAACTCACTGGGGCCTACAGCTTTG 42
              ||||||  | ||||||||   |||| ||||||
Db         96 GCCTCCCAACCTCACTGGCTACTACCGCTTTG 127


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Title: US-09-801-371A-2
Perfect score: 43
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	43	100.0	43	21	AAZ99817	Cis-acting nucleot
	2	43	100.0	50	21	AAZ99815	Sequence of the st
	3	43	100.0	104	21	AAZ99816	Cis-acting nucleot
	4	43	100.0	787	20	AAZ20979	Human TNFalpha 3'U
	5	43	100.0	815	8	AAN70075	Human anti-tumor p
	6	43	100.0	817	11	AAQ04340	THP-1. Homo sapie
	7	43	100.0	818	10	AAN91035	XhoI - PstI sectio
	8	43	100.0	1200	8	AAN70072	Human anti-tumor p
	9	43	100.0	1200	10	AAN90969	Part of gene for a
	10	43	100.0	1275	7	AAN60558	Sequence encoding
	11	43	100.0	1323	7	AAN60363	Sequence encoding
	12	43	100.0	1324	21	AAF21085	Human low adenosin
	13	43	100.0	1324	21	AAA34963	Human adenosine re
	14	43	100.0	1560	9	AAN80219	Sequence of pE4 en
	15	43	100.0	1585	7	AAN60557	Sequence encoding
	16	43	100.0	1585	7	AAN60527	Sequence encoding
	17	43	100.0	1606	7	AAN60446	Sequence encoding
	18	43	100.0	1606	17	AAT15424	Human tumour necro
	19	43	100.0	1643	8	AAN71307	Sequence encoding
	20	43	100.0	1643	17	AAT31021	Human tumour necro
	21	43	100.0	1643	24	ABK13195	Human tumour necro
	22	43	100.0	1643	25	AAD49644	Human tumour necro
	23	43	100.0	1643	25	AAL53712	Tumour necrosis fa
	24	43	100.0	2270	20	AAZ20983	Chimeric nucleic a
	25	43	100.0	2570	20	AAZ20984	Chimeric nucleic a
	26	43	100.0	3634	19	AAV39005	TNF-alpha gene use
	27	43	100.0	3634	20	AAX09014	Tumour necrosis fa
	28	43	100.0	3634	21	AAC63770	Human TNF-alpha ge
	29	43	100.0	3634	21	AAA40760	Human tumour necro
	30	43	100.0	6911	24	AAD45858	Human tumour necro
	31	43	100.0	6911	24	AAD45898	Human tumour necro
	32	43	100.0	7112	22	AAF86085	Lymphotoxin and tu
	33	43	100.0	7112	22	AAF57450	Human tumour necro
	34	43	100.0	7112	25	AAL51863	Human tumour necro
c	35	43	100.0	16310	21	AAF21086	Human low adenosin
c	36	43	100.0	16310	21	AAA34964	Human adenosine re
	37	43	100.0	17634	21	AAF21087	Human low adenosin
c	38	43	100.0	17634	21	AAF21087	Human low adenosin
	39	43	100.0	17634	21	AAA34965	Human adenosine re
c	40	43	100.0	17634	21	AAA34965	Human adenosine re
c	41	43	100.0	81800	24	ABK84756	Human cDNA differe
	42	41.4	96.3	1585	15	AAQ58037	Tumor necrosis fac
	43	30.6	71.2	51	21	AAZ99916	Sequence of the st
	44	24.6	57.2	811	13	AAQ22830	Sequence encoding
	45	24.6	57.2	1678	13	AAQ22829	Sequence encoding

ALIGNMENTS

RESULT 1
AAZ99817
ID AAZ99817 standard; RNA; 43 BP.
XX
AC AAZ99817;
XX
DT 12-JUL-2000 (first entry)
XX
DE Cis-acting nucleotide sequence derived from human TNF-alpha.
XX
KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200014255-A1.
XX
PD 16-MAR-2000.
XX
PF 06-SEP-1999; 99WO-IL00483.
XX
PR 07-SEP-1998; 98IL-0126112.
PR 26-OCT-1998; 98IL-0126757.
XX
PA (YISS) YISSUM RES & DEV CO.
XX
PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
XX
DR WPI; 2000-257000/22.
XX

PT Regulation of gene expression by mRNA splicing is carried out using a
PT cis-acting nucleotide sequence controlled by phosphorylation of the
PT alpha-subunit of eukaryotic initiation factor 2 -
XX
PS Claim 5; Page 15; 75pp; English.
XX
CC The specification describes a cis-acting nucleotide sequence which is
CC capable of removing introns from a precursor transcript encoded by a
CC gene which harbours at least one cis-acting nucleotide sequence. This
CC removal is effected during the production of mRNA of the gene, and
CC depends on activation of a trans-acting factor which is an RNA-activated
CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic
CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
CC sequence, derived from the 3' untranslated region (3'UTR) of the human
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
CC splicing of precursor transcripts encoded by that gene sensitive to the
CC level of RNA-activated protein kinase (PKR) activity. The sequence can
CC be used to transform host cells to regulate gene expression at the mRNA
CC splicing level, for gene therapy, and to produce a recombinant
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC protein) or industrially or agriculturally applicable protein. The
CC present sequence represents a cis-acting nucleotide sequence of the
CC invention.
XX
SQ Sequence 43 BP; 10 A; 13 C; 11 G; 9 T; 0 other;

Query Match 100.0%; Score 43; DB 21; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
||||||||||||||||||||||||||||||||||||||||||||
Db 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43

RESULT 2
AAZ99815
ID AAZ99815 standard; RNA; 50 BP.
XX
AC AAZ99815;
XX
DT 12-JUL-2000 (first entry)
XX
DE Sequence of the stem loop of tumour necrosis factor-alpha gene.
XX
KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200014255-A1.
XX
PD 16-MAR-2000.
XX
PF 06-SEP-1999; 99WO-IL00483.
XX
PR 07-SEP-1998; 98IL-0126112.
PR 26-OCT-1998; 98IL-0126757.
XX
PA (YISS) YISSUM RES & DEV CO.
XX
PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
XX
DR WPI; 2000-257000/22.
XX
PT Regulation of gene expression by mRNA splicing is carried out using a
PT cis-acting nucleotide sequence controlled by phosphorylation of the
PT alpha-subunit of eukaryotic initiation factor 2 -
XX
PS Example 7; Fig 5B; 75pp; English.
XX
CC The specification describes a cis-acting nucleotide sequence which is
CC capable of removing introns from a precursor transcript encoded by a
CC gene which harbours at least one cis-acting nucleotide sequence. This
CC removal is effected during the production of mRNA of the gene, and
CC depends on activation of a trans-acting factor which is an RNA-activated
CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic
CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
CC sequence, derived from the 3' untranslated region (3'UTR) of the human
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
CC splicing of precursor transcripts encoded by that gene sensitive to the
CC level of RNA-activated protein kinase (PKR) activity. The sequence can
CC be used to transform host cells to regulate gene expression at the mRNA
CC splicing level, for gene therapy, and to produce a recombinant
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC protein) or industrially or agriculturally applicable protein. The
CC present sequence represents a fragment of the 3'UTR of human TNF-alpha.
XX
SQ Sequence 50 BP; 12 A; 15 C; 12 G; 11 U; 0 other;

Query Match 100.0%; Score 43; DB 21; Length 50;
Best Local Similarity 79.1%; Pred. No. 2e-07;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
:|||||:||||||:||||||||:|||:||||||:|||||:::||
Db 5 UCAAACUGGGGCCUCCAGAACUCACUGGGGCCUACAGCUUUGA 47

RESULT 3
AAZ99816
ID AAZ99816 standard; RNA; 104 BP.
XX
AC AAZ99816;
XX
DT 12-JUL-2000 (first entry)
XX
DE Cis-acting nucleotide sequence derived from human TNF-alpha.
XX
KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200014255-A1.
XX
PD 16-MAR-2000.
XX
PF 06-SEP-1999; 99WO-IL00483.
XX
PR 07-SEP-1998; 98IL-0126112.
PR 26-OCT-1998; 98IL-0126757.
XX
PA (YISS) YISSUM RES & DEV CO.
XX
PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
XX
DR WPI; 2000-257000/22.
XX
PT Regulation of gene expression by mRNA splicing is carried out using a
PT cis-acting nucleotide sequence controlled by phosphorylation of the
PT alpha-subunit of eukaryotic initiation factor 2 -
XX
PS Claim 4; Page 15; 75pp; English.
XX
CC The specification describes a cis-acting nucleotide sequence which is
CC capable of removing introns from a precursor transcript encoded by a
CC gene which harbours at least one cis-acting nucleotide sequence. This
CC removal is effected during the production of mRNA of the gene, and
CC depends on activation of a trans-acting factor which is an RNA-activated
CC protein kinase capable of phosphorylating the alpha-subunit of eukaryotic
CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
CC sequence, derived from the 3' untranslated region (3'UTR) of the human
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders

CC splicing of precursor transcripts encoded by that gene sensitive to the
CC level of RNA-activated protein kinase (PKR) activity. The sequence can
CC be used to transform host cells to regulate gene expression at the mRNA
CC splicing level, for gene therapy, and to produce a recombinant
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC protein) or industrially or agriculturally applicable protein. The
CC present sequence represents a cis-acting nucleotide sequence of the
CC invention.
XX
SQ Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 other;

Query Match 100.0%; Score 43; DB 21; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
||||||||||||||||||||||||||||||||||||||||||||
Db 5 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 47

RESULT 4
AAZ20979
ID AAZ20979 standard; DNA; 787 BP.
XX
AC AAZ20979;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human TNFalpha 3'UTR.
XX
KW TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW psoriasis; graft versus host disease; lupus erythematosus;
KW diabetes; ankylosing spondylitis; rheumatoid arthritis; ds.
XX
OS Homo sapiens.
XX
PN WO9943840-A1.
XX
PD 02-SEP-1999.
XX
PF 12-JAN-1999; 99WO-US00637.
XX
PR 27-FEB-1998; 98US-0076316.
XX
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Tatake RJ, Marlin SD, Barton RW;
XX
DR WPI; 1999-527630/44.
XX
PT A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)
PT promoter and an apoptosis-inducing Granzyme B polynucleotide -
XX
PS Example 1; Page 60-61; 71pp; English.
XX
CC This sequence represents a human TNFalpha (tumour necrosis factor alpha)
CC 3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984)
CC were constructed comprising at least one TNFalpha promoter enhancer
CC region (AAZ20975-Z20978), a TNFalpha promoter (AAZ20972-Z20974), a DNA
CC encoding the apoptosis-inducing Granzyme B protein (AAZ20982), and a
CC TNFalpha 3'UTR sequence. TNFalpha is one of a number of
CC cytokines produced by inflammatory cells. Upregulation and/or
CC dysregulation of cytokines in inflamed tissue may be directly or
CC indirectly responsible for exacerbation of chronic inflammatory
CC diseases. Introduction of the chimeric nucleotide to activated
CC inflammatory cells causes them to undergo apoptosis. Pharmaceutical
CC compositions of the chimeric nucleotide may be useful for treating
CC inflammatory disorders such as multiple sclerosis, Crohn's disease,
CC ulcerative colitis, psoriasis, graft versus host disease, lupus
CC erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing
CC spondylitis, and in particular, rheumatoid arthritis. The use of such
CC chimeric nucleotides offers simpler and cheaper long-term relief, in
CC comparison with existing conventional pharmaceutical and invasive surgery
CC methods.
XX
SQ Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 other;

Query Match 100.0%; Score 43; DB 20; Length 787;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
||||||||||||||||||||||||||||||||||||||||||||
Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268

RESULT 5
AAN70075
ID AAN70075 standard; DNA; 815 BP.
XX
AC AAN70075;
XX
DT 25-MAR-2003 (updated)
DT 20-JAN-1991 (first entry)
XX
DE Human anti-tumor polypeptide Xho-PstI fragment.
XX
KW Anti-tumor; cancer; cytotoxic; ss.
XX
OS Homo sapiens.
XX
PN EP247906-A.
XX
PD 02-DEC-1987.
XX
PF 04-FEB-1987; 87EP-0400261.
XX
PR 04-FEB-1986; 86JP-0021302.
PR 07-FEB-1986; 86JP-0024220.
PR 17-JUL-1986; 86JP-0169522.
XX
PA (MIZU/) MIZUNO D.
XX
PI Mizuno D;
PI Soma GI;
XX
DR WPI; 1987-336540/48.
XX
PT Anti-tumor polypeptides - prepared using recombinant DNA prepared
PT from genomic DNA of human acute leukemia cell THP-1.
XX
PS Disclosure; Fig 7; 63pp; English.
XX
CC The sequence is an Xho-PstI fragment of an anti-tumor protein.
CC The polypeptide is cytotoxic to human tumor cells but not to normal
CC cells. They are also cytotoxic to primary cell cultures obtained
CC from metastasis lesions of patients suffering from striated muscle
CC tumors. They are also resistant to all chemotherapeutic agents.
CC See also AAN70073-74, AAP70077-78 and AAP95592.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 815 BP; 183 A; 267 C; 205 G; 160 T; 0 other;

Query Match 100.0%; Score 43; DB 8; Length 815;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
||||||||||||||||||||||||||||||||||||||||||||
Db 716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758

RESULT 6
AAQ04340
ID AAQ04340 standard; DNA; 817 BP.

```
XX
AC   AAQ04340;
XX
DT   25-MAR-2003  (updated)
DT   21-SEP-1990  (first entry)
XX
DE   THP-1.
XX
KW   Acute leukaemia cell; THP-1; anti-tumour agent; ss.
XX
OS   Homo sapiens.
XX
PN   JP02088598-A.
XX
PD   28-MAR-1990.
XX
PF   22-SEP-1988;   88JP-0239154.
XX
PR   22-SEP-1988;   88JP-0239154.
XX
PA   (SOMA/) SOMA G.
XX
DR   WPI; 1990-143138/19.
XX
PT   Intrinsic TNF prodn. derivation agents - contain primer and trigger,
PT   at least one of which has TNF activity.
XX
PS   Disclosure; Page ?; ?pp; Japanese.
XX
CC   Used in the prodn. of TNF prodn. agents.
CC   (Updated on 25-MAR-2003 to correct PD field.)
XX
SQ   Sequence 817 BP; 183 A; 268 C; 206 G; 160 T; 0 other;

  Query Match            100.0%;  Score 43;  DB 11;  Length 817;
  Best Local Similarity  100.0%;  Pred. No. 3e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758


RESULT 7
AAN91035
ID   AAN91035 standard; DNA; 818 BP.
XX
AC   AAN91035;
XX
DT   11-MAR-1990  (first entry)
XX
DE   XhoI - PstI section of gene for anti-cancer peptide.
XX
KW   Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
XX
OS   THP-1 cells.
XX
PN   JP01095784-A.
XX
PD   13-APR-1989.
XX
PF   06-OCT-1987;   87JP-0252174.
XX
PR   06-OCT-1987;   87JP-0252174.
XX
PA   (SENG/) SEN G.
XX
DR   WPI; 1989-154899/21.
XX
PT   Novel DNA, plasmid and polypeptide(s)
PT   - useful as anticarcinogenic agents
XX
PS   Fig 3; Page ?; 17pp; Japanese.
XX
CC   Section of gene for anticarcinogenic peptide. It is genomic DNA or cDNA
CC   from THP-1 cells.
XX
SQ   Sequence 818 BP; 184 A; 268 C; 206 G; 160 T; 0 other;

  Query Match            100.0%;  Score 43;  DB 10;  Length 818;
  Best Local Similarity  100.0%;  Pred. No. 3e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        717 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 759


RESULT 8
AAN70072
ID   AAN70072 standard; DNA; 1200 BP.
XX
AC   AAN70072;
XX
DT   25-MAR-2003  (updated)
DT   20-JAN-1991  (first entry)
XX
DE   Human anti-tumor polypeptide.
XX
KW   Anti-tumor; cancer; cytotoxic; ss.
XX
OS   Homo sapiens.
XX
PN   EP247906-A.
XX
PD   02-DEC-1987.
XX
PF   04-FEB-1987;   87EP-0400261.
XX
PR   04-FEB-1986;   86JP-0021302.
PR   07-FEB-1986;   86JP-0024220.
PR   17-JUL-1986;   86JP-0169522.
XX
PA   (MIZU/) MIZUNO D.
XX
PI   Mizuno D;
PI   Soma GI;
XX
DR   WPI; 1987-336540/48.
XX
PT   Anti-tumor polypeptides - prepared using recombinant DNA prepared
PT   from genomic DNA of human acute leukemia cell THP-1.
XX
PS   Disclosure; Fig 4; 63pp; English.
XX
CC   The polypeptide is cytotoxic to human tumor cells but not to normal
CC   cells.  They are also cytotoxic to primary cell cultures obtained
CC   from metastasis lesions of patients suffering from striated muscle
CC   tumors.  They are also resistant to all chemotherapeutic agents.
CC   See also AAN70073-75, AAP70077-78 and AAP95592.
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 other;

  Query Match            100.0%;  Score 43;  DB 8;  Length 1200;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db       1099 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1141


RESULT 9
AAN90969
ID   AAN90969 standard; DNA; 1200 BP.
```

XX
AC AAN90969;
XX
DT 25-MAR-2003 (updated)
DT 11-MAR-1990 (first entry)
XX
DE Part of gene for anti-cancer peptide.
XX
KW Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
XX
OS THP-1 cells.
XX
PN JP01095784-A.
XX
PD 13-APR-1989.
XX
PF 06-OCT-1987; 87JP-0252174.
XX
PR 06-OCT-1987; 87JP-0252174.
XX
PA (SENG/) SEN G.
XX
DR WPI; 1989-154899/21.
XX
PT Novel DNA, plasmid and polypeptide(s)
PT - useful as anticarcinogenic agents
XX
PS Fig 2; Page ?; 17pp; Japanese.
XX
CC Gene for anticarcinogenic peptide. It is genomic DNA or cDNA from THP-1
CC cells.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 other;

Query Match 100.0%; Score 43; DB 10; Length 1200;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
||||||||||||||||||||||||||||||||||||||||||||
Db 1099 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1141

RESULT 10
AAN60558
ID AAN60558 standard; DNA; 1275 BP.
XX
AC AAN60558;
XX
DT 28-JUL-1991 (first entry)
XX
DE Sequence encoding mature human tumour necrosis factor (hTNF) mutein
DE Ser 69 in pAW731.
XX
KW Antitumour; anticancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..474
FT /*tag= a
XX
PN WO8604606-A.
XX
PD 14-AUG-1986.
XX
PF 03-FEB-1986; 86WO-US00236.
XX
PR 07-FEB-1985; 85US-0698939.
PR 19-OCT-1982; 82US-0435154.
PR 15-APR-1983; 83US-0486162.
PR 20-DEC-1983; 83US-0564224.
PR 15-OCT-1984; 84US-0661026.
PR 07-FEB-1985; 85US-0695934.
XX
PA (CETU) CETUS CORP.
XX
PI Mark DF, Lin LS, Lu SDY, Wang AM;
XX
DR WPI; 1986-225458/34.
DR P-PSDB; AAP60656.
XX
PT New synthetic muteins of human tumour necrosis factor protein -
PT are obtd. by direct mutagenesis and retain antitumour activity
XX
PS Disclosure; Fig 3a; 47pp; English.
XX
CC The sequence encoding TNF produced by the promyelocytic leukemia
CC cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in
CC E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in
CC the TNF sequence appears to be involved in disulphide linkages. The
CC patentors claim a novel synthetic mutein of a biologically active
CC hTNF protein, having at least one cysteine residue free from a
CC disulphide link and non-essential to the activity and having at
CC least one of the cysteine residues deleted or replaced by another AA.
CC Plasmid pAW731 (Ser 69) is claimed.
XX
SQ Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 other;

Query Match 100.0%; Score 43; DB 7; Length 1275;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
||||||||||||||||||||||||||||||||||||||||||||
Db 697 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 739

RESULT 11
AAN60363
ID AAN60363 standard; DNA; 1323 BP.
XX
AC AAN60363;
XX
DT 19-JUN-1991 (first entry)
XX
DE Sequence encoding human tumour necrosis factor.
XX
KW hTNF; tumour; cancer; interferon; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..534
FT /*tag= a
FT sig_peptide 1..60
FT /*tag= b
FT /label= Secretory leader peptide
FT mat_peptide 61..534
FT /*tag= c
XX
PN EP168214-A.
XX
PD 15-JAN-1986.
XX
PF 03-JUL-1985; 85EP-0304758.
XX
PR 03-DEC-1984; 84US-0677454.
PR 05-JUL-1984; 84US-0627959.
PR 05-JUL-1984; 84US-0628059.
PR 05-JUL-1984; 84US-0628060.
PR 03-DEC-1984; 84US-0677156.
PR 03-DEC-1984; 84US-0677257.
PR 25-JUL-1984; 84US-0627969.
PR 03-DEC-1984; 84US-0677267.

```
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Aggarwal BB,  Lee SH,  Goeddel DV,  Nedwin GE;
XX
DR   WPI; 1986-015483/03.
DR   P-PSDB; AAP60417.
XX
PT   Pure tumour necrosis factor and mutant forms - new DNA coding
PT   sequences and transformed cells.
XX
PS   Claim 20; Fig 10; 90pp; English.
XX
CC   Sequence encodes the pure human tumour necrosis factor, mutants of
CC   which are covered by the claims. TNF and mutants are useful in
CC   treating tumours, especially in tandem with interferon. The
CC   encoding sequence may be used to create plasmid pTrpXAPTNF, allowing
CC   transformation of an E.coli host for the expression of TNF.
XX
SQ   Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 other;

  Query Match             100.0%;  Score 43;  DB 7;  Length 1323;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        754 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 796


RESULT 12
AAF21085
ID   AAF21085 standard; DNA; 1324 BP.
XX
AC   AAF21085;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human low adenosine antisense oligonucleotide related sequence #2652.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
PS   Disclosure; Page 887; 1592pp; English.
XX
CC   The present invention describes low adenosine (A) content antisense
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC   and/or surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotidee used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;

  Query Match             100.0%;  Score 43;  DB 21;  Length 1324;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        755 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 797


RESULT 13
AAA34963
ID   AAA34963 standard; DNA; 1324 BP.
XX
AC   AAA34963;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2652.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US17712.
XX
PR   03-AUG-1998;   98US-0095212.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
```

```
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstriction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers -
XX
PS   Disclosure; Page 814-815; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an
CC   antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC   targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC   asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC   carcinomas, and cancers which may metastasise to the lungs, including
CC   breast and prostate cancer. The reduction of the adenosine content of
CC   the ONs reduces side effects. The A-containing ONs break down with the
CC   release of deoxyadenosine which activates adenosine receptors causing
CC   bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC   nucleotide sequences given in the sequence listing from the present
CC   invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC   185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC   differ from the previously named sequences. SEQ ID NO:11 to 1680
CC   (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC   invention. N.B. Sequences given in the disclosure of the present
CC   invention do not match up with their corresponding SEQ ID NO: sequences
CC   given in the sequence listing.
XX
SQ   Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;

  Query Match           100.0%;  Score 43;  DB 21;  Length 1324;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        755 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 797


RESULT 14
AAN80219
ID   AAN80219 standard; DNA; 1560 BP.
XX
AC   AAN80219;
XX
DT   28-DEC-1990  (first entry)
XX
DE   Sequence of pE4 encoding human tumour necrosis factor (TNF).
XX
KW   Lymphokine; antitumour; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             86..313
FT                   /*tag=  a
FT   mat_peptide     314..787
FT                   /*tag=  b
XX
PN   WO8806625-A.
XX
PD   07-SEP-1988.
XX
PF   25-JAN-1988;   88WO-US00183.
XX
PR   26-FEB-1987;   87US-0019221.
XX
PA   (CETU ) CETUS CORP.
XX
PI   Mark DF,  Thomson JW,  Lin LS,  Yamamoto R;
XX
DR   WPI; 1988-271165/38.
DR   P-PSDB; AAP80728.
XX
PT   Human tumour necrosis factor muteins -
PT   having comparable biological activity with improved stability
PT   and ease of purification
XX
PS   Disclosure; Fig 1-1 to 1-2; 51pp; English.
XX
CC   A human TNF protein which is modified from the sequence shown in
CC   AAP80728, including naturally ocurring allelic variants is claimed. Also
CC   claimed are: recombinant DNA sequences encoding the protein (AAN80219)
CC   and control sequences for expression; a vector; a transformed host cell;
CC   a method of producing the protein by culturing the host cell;
CC   pharmaceutical compsn. of the protein and a carrier and a method of
CC   treating tumour burden with the compsn. The muteins are capable of the
CC   range of biological activities exhibited by native TNF but exhibit
CC   improved stability and ease of purification.
XX
SQ   Sequence 1560 BP; 340 A; 473 C; 381 G; 366 T; 0 other;

  Query Match           100.0%;  Score 43;  DB 9;  Length 1560;
  Best Local Similarity  100.0%;  Pred. No. 3.3e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db       1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049


RESULT 15
AAN60557
ID   AAN60557 standard; DNA; 1585 BP.
XX
AC   AAN60557;
XX
DT   28-JUL-1991  (first entry)
XX
DE   Sequence encoding mature human tumour necrosis factor (hTNF) in pE4.
XX
KW   Antitumour; anticancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             86..313
FT                   /*tag=  a
FT   mat_peptide     314..787
FT                   /*tag=  b
XX
PN   WO8604606-A.
XX
PD   14-AUG-1986.
XX
PF   03-FEB-1986;   86WO-US00236.
XX
PR   07-FEB-1985;   85US-0698939.
PR   19-OCT-1982;   82US-0435154.
PR   15-APR-1983;   83US-0486162.
PR   20-DEC-1983;   83US-0564224.
PR   15-OCT-1984;   84US-0661026.
PR   07-FEB-1985;   85US-0695934.
XX
PA   (CETU ) CETUS CORP.
XX
PI   Mark DF,  Lin LS,  Lu SDY,  Wang AM;
```

XX
DR WPI; 1986-225458/34.
DR P-PSDB; AAP60655.
XX
PT New synthetic muteins of human tumour necrosis factor protein -
PT are obtd. by direct mutagenesis and retain antitumour activity
XX
PS Disclosure; Fig 1; 47pp; English.
XX
CC The sequence encoding TNF produced by the promyelocytic leukemia
CC cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in
CC E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in
CC the TNF sequence appears to be involved in disulphide linkages. The
CC patentors claim a novel synthetic mutein of a biologically active
CC hTNF protein, having at least one cysteine residue free from a
CC disulphide link and non-essential to the activity and having at
CC least one of the cysteine residues deleted or replaced by another AA.
CC Plasmid pAW731 (Ser 69) is claimed.
XX
SQ Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 other;

Query Match 100.0%; Score 43; DB 7; Length 1585;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
||||||||||||||||||||||||||||||||||||||||||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

Search completed: February 3, 2004, 04:47:56
Job time : 120.054 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 3, 2004, 04:34:02 ; Search time 2465.58 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	104	100.0	474	13	BX118951	BX118951 BX118951
c 2	104	100.0	630	14	CB528492	CB528492 UI-H-FT2-
c 3	104	100.0	645	14	CD370363	CD370363 UI-H-FT1-
c 4	104	100.0	688	14	CD367676	CD367676 UI-H-FT1-
c 5	104	100.0	696	14	CA307225	CA307225 UI-H-FT1-
c 6	104	100.0	699	14	CD364761	CD364761 UI-H-FT2-
c 7	104	100.0	703	14	CD368142	CD368142 UI-H-FT1-
c 8	104	100.0	713	14	CA308256	CA308256 UI-H-FT1-
c 9	104	100.0	719	14	CB528694	CB528694 UI-H-FT2-
c 10	104	100.0	722	12	BQ007008	BQ007008 UI-H-EI1-
c 11	104	100.0	722	14	CA307062	CA307062 UI-H-FT1-
c 12	104	100.0	722	14	CD364988	CD364988 UI-H-FT2-
c 13	104	100.0	723	14	CA308777	CA308777 UI-H-FT1-
c 14	104	100.0	723	14	CD368116	CD368116 UI-H-FT1-
c 15	104	100.0	724	14	CA309711	CA309711 UI-H-FT1-
c 16	104	100.0	726	14	CA310368	CA310368 UI-H-FT1-
c 17	104	100.0	726	14	CD368929	CD368929 UI-H-FT1-
c 18	104	100.0	742	14	CA309509	CA309509 UI-H-FT1-
c 19	104	100.0	744	14	CD366187	CD366187 UI-H-FT1-
c 20	104	100.0	748	14	CA306559	CA306559 UI-H-FT1-
c 21	104	100.0	1201	9	AL543083	AL543083 AL543083
22	103	99.0	248	14	T29839	T29839 EST97164 Hu
c 23	103	99.0	693	14	CD367625	CD367625 UI-H-FT1-
c 24	102.4	98.5	684	14	CA307429	CA307429 UI-H-FT1-
c 25	102.4	98.5	713	14	CA309664	CA309664 UI-H-FT1-
c 26	102.4	98.5	718	14	CD367794	CD367794 UI-H-FT1-
c 27	100.8	96.9	672	14	CD367664	CD367664 UI-H-FT1-
c 28	86	82.7	581	9	AI242177	AI242177 qh81g08.x
c 29	85	81.7	561	10	BG232086	BG232086 naf32e06.
c 30	68.2	65.6	583	14	CA748748	CA748748 UI-H-FT1-
c 31	61.4	59.0	1011	9	AL575811	AL575811 AL575811
c 32	61.2	58.8	564	9	AA699697	AA699697 zi78f12.s
c 33	60.8	58.5	562	9	AA207062	AA207062 zr87b03.s
c 34	48.2	46.3	546	9	AA824594	AA824594 oc83d11.s
35	34.8	33.5	136	28	B38591	B38591 HS-1047-B2-
c 36	32.6	31.3	691	9	AL110410	AL110410 DKFZp434K
c 37	32.6	31.3	888	13	BQ232100	BQ232100 AGENCOURT
c 38	32.2	31.0	342	10	BF407522	BF407522 UI-R-BJ2-
39	31.8	30.6	876	29	CNS00IYJ	AL075400 Drosophil
40	30.4	29.2	430	14	CA563031	CA563031 K0308C04-
41	30.4	29.2	446	10	BB840094	BB840094 BB840094
42	30.4	29.2	452	9	AI286591	AI286591 uk04d09.y
43	30.4	29.2	480	14	CA568528	CA568528 K0428H07-
44	30.4	29.2	497	14	CA564319	CA564319 K0324G08-
45	30.4	29.2	504	14	CA563286	CA563286 K0312B07-

ALIGNMENTS

RESULT 1
BX118951
LOCUS BX118951 474 bp mRNA linear EST 10-FEB-2003
DEFINITION BX118951 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGp998L124300 ; IMAGE:1693595, mRNA sequence.
ACCESSION BX118951
VERSION BX118951.1 GI:27882696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 474)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.
TITLE Human UnigeneSet - RZPD3
JOURNAL Unpublished
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998L124300.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany

```
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES              Location/Qualifiers
     source           1. .474
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGp998L124300 ; IMAGE:1693595"
                      /sex="unknown"
                      /dev_stage="19 weeks"
                      /lab_host="DH10B (ampicillin resistant)"
                      /clone_lib="Soares_fetal_heart_NbHH19W"
                      /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was size selected, ligated to Eco RI
                      adapters (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of a modified pT7T3 vector
                      (Pharmacia). Library went through one round of
                      normalization to a Cot = 5. Library constructed by
                      M.Fatima Bonaldo. This library was constructed from the
                      same fetus as the fetal lung library, Soares fetal lung
                      NbHL19W."
BASE COUNT      112 a    118 c    113 g    131 t
ORIGIN

  Query Match             100.0%;  Score 104;  DB 13;  Length 474;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-21;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 124

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db        125 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 168


RESULT 2
CB528492/c
LOCUS       CB528492                 630 bp    mRNA    linear   EST 16-MAY-2003
DEFINITION  UI-H-FT2-bjd-e-20-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
            UI-H-FT2-bjd-e-20-0-UI 3', mRNA sequence.
ACCESSION   CB528492
VERSION     CB528492.1  GI:29388228
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 630)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 1-29, >AT_rich#Low_complexity (matched compliment)
            205-279, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .630
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="UI-H-FT2-bjd-e-20-0-UI"
                      /tissue_type="Aveolar Macrophage"
                      /dev_stage="Adult"
                      /lab_host="DH10B (Life Technologies)"
                      /clone_lib="NCI_CGAP_FT2"
                      /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                      modified polylinker; Site_1: EcoR I; Site_2: Not I;
                      NCI_CGAP_FT2 is a subtracted cDNA library constructed from
                      a pool of 81 RNA samples from Alveolar Macrophages
                      challenged with different treatments. The library was
                      subtracted according to Bonaldo, Lennon and Soares, Genome
                      Research, 6:791-806, 1996. The tissue was provided by Dr.
                      Gary W. Hunninghake of the University of Iowa.
                      TAG_LIB=UI-H-FT2
                      TAG_TISSUE=Human Lung Aveolar Macrophage
                      TAG_SEQ=GGCCATGCCG"
BASE COUNT      180 a    137 c    139 g    174 t
ORIGIN

  Query Match             100.0%;  Score 104;  DB 14;  Length 630;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-21;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 444

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db        443 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 400


RESULT 3
CD370363/c
LOCUS       CD370363                 645 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  UI-H-FT1-bkb-n-03-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bkb-n-03-0-UI 3', mRNA sequence.
ACCESSION   CD370363
VERSION     CD370363.1  GI:31154453
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 645)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 294-368, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .645
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="UI-H-FT1-bkb-n-03-0-UI"
```

```
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT1
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      191 a    145 c    144 g    165 t
ORIGIN

  Query Match             100.0%;  Score 104;  DB 14;  Length 645;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-21;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 533

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db        532 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 489


RESULT 4
CD367676/c
LOCUS       CD367676                688 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  UI-H-FT1-bjr-l-14-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bjr-l-14-0-UI 3', mRNA sequence.
ACCESSION   CD367676
VERSION     CD367676.1  GI:31151766
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 688)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 69-143, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .688
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bjr-l-14-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT1
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      176 a    148 c    181 g    183 t
ORIGIN

  Query Match             100.0%;  Score 104;  DB 14;  Length 688;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-21;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 308

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db        307 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 264


RESULT 5
CA307225/c
LOCUS       CA307225                696 bp    mRNA    linear   EST 01-NOV-2002
DEFINITION  UI-H-FT1-bhu-n-04-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bhu-n-04-0-UI 3', mRNA sequence.
ACCESSION   CA307225
VERSION     CA307225.1  GI:24470279
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 696)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 296-370, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .696
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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```
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bhu-n-04-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT1
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      198 a    155 c    160 g    181 t      2 others
ORIGIN

  Query Match             100.0%;  Score 104;  DB 14;  Length 696;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-21;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 535

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        534 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 491


RESULT 6
CD364761/c
LOCUS       CD364761                699 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  UI-H-FT2-bjm-j-11-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
            UI-H-FT2-bjm-j-11-0-UI 3', mRNA sequence.
ACCESSION   CD364761
VERSION     CD364761.1  GI:31148851
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 699)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 296-370, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .699
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT2-bjm-j-11-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT2"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT2 is a subtracted cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     subtracted according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. The tissue was provided by Dr.
                     Gary W. Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT2
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      200 a    157 c    160 g    182 t
ORIGIN

  Query Match             100.0%;  Score 104;  DB 14;  Length 699;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-21;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 535

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        534 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 491


RESULT 7
CD368142/c
LOCUS       CD368142                703 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  UI-H-FT1-bjv-e-20-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bjv-e-20-0-UI 3', mRNA sequence.
ACCESSION   CD368142
VERSION     CD368142.1  GI:31152232
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 703)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 298-372, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .703
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bjv-e-20-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
```

```
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT1
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      197 a    158 c    161 g    185 t      2 others
ORIGIN

  Query Match             100.0%;  Score 104;  DB 14;  Length 703;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-21;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 537

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        536 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 493


RESULT 8
CA308256/c
LOCUS       CA308256                713 bp    mRNA    linear   EST 01-NOV-2002
DEFINITION  UI-H-FT1-bhy-e-14-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bhy-e-14-0-UI 3', mRNA sequence.
ACCESSION   CA308256
VERSION     CA308256.1  GI:24471310
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 713)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 296-370, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .713
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bhy-e-14-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT1
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      203 a    164 c    161 g    184 t      1 others
ORIGIN

  Query Match             100.0%;  Score 104;  DB 14;  Length 713;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-21;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 535

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        534 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 491


RESULT 9
CB528694/c
LOCUS       CB528694                719 bp    mRNA    linear   EST 16-MAY-2003
DEFINITION  UI-H-FT2-bjd-l-22-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
            UI-H-FT2-bjd-l-22-0-UI 3', mRNA sequence.
ACCESSION   CB528694
VERSION     CB528694.1  GI:29388630
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 719)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 294-368, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .719
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT2-bjd-l-22-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
```

/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_LIB=UI-H-FT2
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"
BASE COUNT 203 a 163 c 163 g 188 t 2 others
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 719;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 592 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 533

Qy 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
Db 532 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 489

RESULT 10
BQ007008/c
LOCUS BQ007008 722 bp mRNA linear EST 26-MAR-2002
DEFINITION UI-H-EI1-azb-j-22-0-UI.s1 NCI_CGAP_EI1 Homo sapiens cDNA clone IMAGE:5846517 3', mRNA sequence.
ACCESSION BQ007008
VERSION BQ007008.1 GI:19731908
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 722)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5846517"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_EI1"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_EI1 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACACTTGCAC.
TAG_LIB=UI-H-EI1
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTTGCAC"
BASE COUNT 204 a 162 c 164 g 190 t 2 others
ORIGIN

Query Match 100.0%; Score 104; DB 12; Length 722;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 595 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536

Qy 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
Db 535 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 492

RESULT 11
CA307062/c
LOCUS CA307062 722 bp mRNA linear EST 01-NOV-2002
DEFINITION UI-H-FT1-bhu-o-04-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone UI-H-FT1-bhu-o-04-0-UI 3', mRNA sequence.
ACCESSION CA307062
VERSION CA307062.1 GI:24470116
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 722)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 295-369, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhu-o-04-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome

Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_LIB=UI-H-FT1
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"
BASE COUNT 203 a 165 c 163 g 189 t 2 others
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 722;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 534

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db        533 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 490
```

RESULT 12
CD364988/c
LOCUS CD364988 722 bp mRNA linear EST 29-MAY-2003
DEFINITION UI-H-FT2-bjn-c-04-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone UI-H-FT2-bjn-c-04-0-UI 3', mRNA sequence.
ACCESSION CD364988
VERSION CD364988.1 GI:31149078
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 722)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjn-c-04-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_LIB=UI-H-FT2
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"
BASE COUNT 201 a 166 c 163 g 190 t 2 others
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 722;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db        535 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 492
```

RESULT 13
CA308777/c
LOCUS CA308777 723 bp mRNA linear EST 01-NOV-2002
DEFINITION UI-H-FT1-bhy-b-23-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone UI-H-FT1-bhy-b-23-0-UI 3', mRNA sequence.
ACCESSION CA308777
VERSION CA308777.1 GI:24471831
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 723)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .723
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhy-b-23-0-UI"
/tissue_type="Aveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag

```
                 sequence that is located between the Not I site and the
                 (dT)18 tail. The sequence tag for this library is
                 GGCCATGCCG. The tissue was provided by Dr. Gary W.
                 Hunninghake of the University of Iowa.
                 TAG_LIB=UI-H-FT1
                 TAG_TISSUE=Human Lung Aveolar Macrophage
                 TAG_SEQ=GGCCATGCCG"
BASE COUNT      203 a    164 c    164 g    191 t      1 others
ORIGIN

  Query Match            100.0%;  Score 104;  DB 14;  Length 723;
  Best Local Similarity  100.0%;  Pred. No. 6.6e-21;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
                ||||||||||||||||||||||||||||||||||||||||||||
Db        535 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 492


RESULT 14
CD368116/c
LOCUS       CD368116                 723 bp    mRNA    linear   EST 29-MAY-2003
DEFINITION  UI-H-FT1-bjv-a-04-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bjv-a-04-0-UI 3', mRNA sequence.
ACCESSION   CD368116
VERSION     CD368116.1  GI:31152206
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 723)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 297-371, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..723
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bjv-a-04-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_LIB=UI-H-FT1
                     TAG_TISSUE=Human Lung Aveolar Macrophage
                     TAG_SEQ=GGCCATGCCG"
BASE COUNT      205 a    164 c    164 g    190 t
ORIGIN

  Query Match            100.0%;  Score 104;  DB 14;  Length 723;
  Best Local Similarity  100.0%;  Pred. No. 6.6e-21;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
                ||||||||||||||||||||||||||||||||||||||||||||
Db        535 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 492


RESULT 15
CA309711/c
LOCUS       CA309711                 724 bp    mRNA    linear   EST 01-NOV-2002
DEFINITION  UI-H-FT1-bic-b-17-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bic-b-17-0-UI 3', mRNA sequence.
ACCESSION   CA309711
VERSION     CA309711.1  GI:24472765
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 724)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 297-371, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1..724
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bic-b-17-0-UI"
                     /tissue_type="Aveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
```

pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_LIB=UI-H-FT1
TAG_TISSUE=Human Lung Aveolar Macrophage
TAG_SEQ=GGCCATGCCG"

BASE COUNT 203 a 166 c 164 g 190 t 1 others
ORIGIN

Query Match 100.0%; Score 104; DB 14; Length 724;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        535 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 492
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Search completed: February 3, 2004, 06:12:17
Job time : 2472.58 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 3, 2004, 03:36:36 ; Search time 450.769 Seconds
(without alignments)
3902.476 Million cell updates/sec

Title: US-09-801-371A-2
Perfect score: 43
Sequence: 1 tcaaactggggcctccagaa.....actggggcctacagctttga 43

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	100.0	400	11	G13533	G13533 SHGC-11076
2	43	100.0	787	6	AR300453	AR300453 Sequence
3	43	100.0	787	6	BD070551	BD070551 Self-regu
4	43	100.0	787	6	BD137681	BD137681 Self-regu
5	43	100.0	817	6	A16444	A16444 Xho-PstI fr
6	43	100.0	817	6	E02109	E02109 DNA sequenc
7	43	100.0	1047	9	HSA249755	AJ249755 Homo sapi
8	43	100.0	1275	6	I08430	I08430 Sequence 5
9	43	100.0	1323	6	I07953	I07953 Sequence 6
10	43	100.0	1324	6	E00702	E00702 cDNA encodi
11	43	100.0	1324	6	I03610	I03610 Sequence 2
12	43	100.0	1379	12	SYNTNFTRP	M35592 Synthetic h
13	43	100.0	1465	6	I04244	I04244 Sequence 2
14	43	100.0	1560	6	I08863	I08863 Sequence 3
15	43	100.0	1585	6	A37272	A37272 Sequence 12
16	43	100.0	1585	6	I04169	I04169 Sequence 1
17	43	100.0	1585	6	I04198	I04198 Sequence 1
18	43	100.0	1585	6	I08384	I08384 Sequence 5
19	43	100.0	1585	6	I08429	I08429 Sequence 3
20	43	100.0	1585	9	HUMTNFAA	M10988 Human tumor
21	43	100.0	1606	6	I07541	I07541 Sequence 22
22	43	100.0	1643	6	AR146199	AR146199 Sequence
23	43	100.0	1643	9	HSTNFR	X01394 Human mRNA
24	43	100.0	1676	9	BC028148	BC028148 Homo sapi
25	43	100.0	2270	6	AR300459	AR300459 Sequence
26	43	100.0	2270	6	BD137687	BD137687 Self-regu
27	43	100.0	2570	6	AR300460	AR300460 Sequence
28	43	100.0	2570	6	BD137688	BD137688 Self-regu
29	43	100.0	3103	9	HUMTNFX	M26331 Human tumor
30	43	100.0	3634	6	AR100270	AR100270 Sequence
31	43	100.0	3634	6	AR149925	AR149925 Sequence
32	43	100.0	3634	6	BD064008	BD064008 Novel exp
33	43	100.0	3634	9	HSTNFA	X02910 Human gene
34	43	100.0	4830	9	AY066019	AY066019 Homo sapi
35	43	100.0	6974	9	AB088112	AB088112 Homo sapi
36	43	100.0	7112	6	AX100950	AX100950 Sequence
37	43	100.0	7112	6	AX100965	AX100965 Sequence
38	43	100.0	7112	9	HUMTNFAB	M16441 Human tumor
39	43	100.0	7240	9	AY214167	AY214167 Homo sapi
c 40	43	100.0	16310	9	HSTNFABX	Z15026 Homo sapien
41	43	100.0	40160	9	BX248519	BX248519 Human DNA
42	43	100.0	61358	9	AL929587	AL929587 Human DNA
c 43	43	100.0	81800	9	HSY14768	Y14768 Homo sapien
c 44	43	100.0	100000	9	AP000505	AP000505 Homo sapi
45	43	100.0	132330	9	AL662801	AL662801 Human DNA

ALIGNMENTS

RESULT 1
G13533
LOCUS G13533 400 bp DNA linear STS 30-MAR-2000
DEFINITION SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G13533
VERSION G13533.1 GI:1129272
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Olivier,M. and Cox,D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)

```
COMMENT
            Contact: Michael Olivier, David R. Cox
            Stanford Human Genome Center
            Stanford University School of Medicine
            4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
            Tel: (650) 320-5800
            Fax: (650) 320-5801
            Email: olivier@shgc.stanford.edu
            Primer A: CACTAAGAATTCAAACTGGGGC
            Primer B: GAGGAAGGCCTAAGGTCCAC
            STS size: 166
            PCR Profile:
                    Initial incubation: 94 degrees C for 90 seconds

                    Denaturation:       94 degrees C for 15 seconds
                    Annealing:          62 degrees C for 23 seconds
                    Polymerization:     72 degrees C for 30 seconds
                    PCR Cycles:         30
                    Thermal Cycler:     Perkin Elmer 9600
            Protocol:
                    Template:       25 ng
                    Primer:         each 1 uM
                    dNTPs:          each 200 uM
                    Taq Polymerase: 0.05 units/ul
                    Total Vol:      10 ul

            Buffer:
                    MgCl2:          2.5 mM
                    KCl:            50  mM
                    Tris-HCl:       20  mM
                    pH:             8.3

            Prepared with primer pairs derived from M10988 -- Unigene.
FEATURES             Location/Qualifiers
     source          1. .400
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="6"
                     /clone_lib="Human"
     STS             210. .375
     primer_bind     210. .231
     primer_bind     complement(356. .375)
BASE COUNT      104 a    120 c     87 g     89 t
ORIGIN

  Query Match             100.0%;  Score 43;  DB 11;  Length 400;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        220 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 262


RESULT 2
AR300453
LOCUS       AR300453                 787 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 7 from patent US 6537784.
ACCESSION   AR300453
VERSION     AR300453.1  GI:31687895
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 787)
  AUTHORS   Tatake,R.J., Marlin,S.D. and Barton,R.W.
  TITLE     Self-regulated apoptosis of inflammatory cells by gene therapy
  JOURNAL   Patent: US 6537784-A 7 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .787
                     /organism="unknown"
BASE COUNT      190 a    204 c    172 g    221 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 6.3e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268


RESULT 3
BD070551
LOCUS       BD070551                 787 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Self-regulated apoptosis of inflammatory cells by gene therapy.
ACCESSION   BD070551
VERSION     BD070551.1  GI:22616154
KEYWORDS    JP 2001516210-A/13.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 787)
  AUTHORS   Tatake,R.J., Marlin,S.D. and Barton,R.W.
  TITLE     Self-regulated apoptosis of inflammatory cells by gene therapy
  JOURNAL   Patent: JP 2001516210-A 13 25-SEP-2001;
            BOEHRINGER INGELHEIM PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2001516210-A/13
            PD   25-SEP-2001
            PF   27-FEB-1998 JP 1998537909
            PR   28-FEB-1997 US    60/039266
            PI   REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC
            A61K31/70,C07H21/04,C12N15/12,C12P19/34
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   TNF alpha nontranslated region
            FH   Key             Location/Qualifiers
            FT   source          1. .787
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .787
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                     /db_xref="taxon:32644"
BASE COUNT      190 a    204 c    172 g    221 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 6.3e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268


RESULT 4
BD137681
LOCUS       BD137681                 787 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Self-regulated apoptosis of inflammatory cells by gene therapy.
ACCESSION   BD137681
VERSION     BD137681.1  GI:23232626
KEYWORDS    JP 2002504381-A/7.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 787)
  AUTHORS   Tatake,R.J., Marlin,S.D. and Barton,R.W.
  TITLE     Self-regulated apoptosis of inflammatory cells by gene therapy
  JOURNAL   Patent: JP 2002504381-A 7 12-FEB-2002;
            BOEHRINGER INGELHEIM PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
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            PN   JP 2002504381-A/7
            PD   12-FEB-2002
            PF   12-JAN-1999 JP 2000533579
            PR   27-FEB-1998 US    60/076316
            PI   REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC
            C12N15/09,A61K31/7088,A61K48/00,A61P1/04,A61P3/10,A61P17/06, PC
            A61P25/00,
            PC   A61P29/00,A61P43/00,C12N9/64,C12Q1/68//C12N5/10,C12N15/00, PC
             C12N5/00
            CC   TNF-alpha untranslated region
            FH   Key             Location/Qualifiers
            FT   source          1. .787
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .787
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      190 a    204 c    172 g    221 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 6.3e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268


RESULT 5
A16444
LOCUS       A16444                   817 bp    DNA     linear   PAT 05-OCT-1994
DEFINITION  Xho-PstI fragment from THP-I cells.
ACCESSION   A16444
VERSION     A16444.1  GI:641014
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 817)
  AUTHORS   Soma,G.I., Mizuno,D., Tsuji,Y. and Kobayashi,N.
  TITLE     Anti-aids preparation
  JOURNAL   Patent: EP 0450240-A 9 09-OCT-1991;
            Soma, Gen-Ichiro; Mizuno, Den'ichi
FEATURES             Location/Qualifiers
     source          1. .817
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      183 a    268 c    206 g    160 t
ORIGIN

  Query Match             100.0%;  Score 43;  DB 6;  Length 817;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758


RESULT 6
E02109
LOCUS       E02109                   817 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA sequence coding for anti-turmor polypeptide.
ACCESSION   E02109
VERSION     E02109.1  GI:2170351
KEYWORDS    JP 1989256390-A/1.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 817)
  AUTHORS   Soma,G., Mizuno,D. and Tsuji,Y.
  TITLE     NOVEL DNA AND PRODUCTION THEREOF, NOVEL PLASMID HAVING SAME, NOVEL
            POLYPEPTIDE AND PRODUCTION THEREOF AND NOVEL ANTINEOPLASTIC AGENT
            FROM SAID POLYPEPTIDE
  JOURNAL   Patent: *JP 1989256390-A 1 12-OCT-1989;
            SOMA GENICHIRO, MIZUNO DENICHI
COMMENT     PN   JP 1989256390-A/1
            PD   12-OCT-1989
            PF   03-APR-1988 JP 1988081683
            PI   SOMA GENICHIRO, MIZUNO DENICHI, TSUJI YOSHIAKI PC
            C12N15/00,A61K37/24,C07K13/00,C12P21/02,(C12P21/02,C12R1:19); CC
            strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            CC   *source: library=THP-1 cell;
            FH   Key             Location/Qualifiers
            FH
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            FT                   /product='Anti-tumor polypeptide'.
FEATURES             Location/Qualifiers
     source          1. .817
                     /organism="Glycine max"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3847"
BASE COUNT      183 a    268 c    206 g    160 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 6.2e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758


RESULT 7
HSA249755
LOCUS       HSA249755               1047 bp    DNA     linear   PRI 29-SEP-1999
DEFINITION  Homo sapiens TNF-alpha gene for tumor necrosis factor-alpha, 3'
            UTR, country United Arab Emirates.
ACCESSION   AJ249755
VERSION     AJ249755.1  GI:6002308
KEYWORDS    TNF-alpha gene; tumor necrosis factor-alpha.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Farhan,A.J., Pravica,V. and Hutchinson,I.V.
  TITLE     Identification of new rare variant of human TNF-alpha 3' UTR
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1047)
  AUTHORS   Farhan,A.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1999) Farhan A.J., CID-Immunology Research
            Division, Manchester University, Medical School, Stopford Building,
            Oxford Road, Manchester, M13 9PT, UNITED KINGDOM
FEATURES             Location/Qualifiers
     source          1. .1047
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /country="United Arab Emirates"
                     /note="new rare variant"
     gene            1. .1047
                     /gene="TNF-alpha"
     3'UTR           1. .>1047
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                     /gene="TNF-alpha"
     variation       322
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                     /replace="t"
BASE COUNT      260 a    282 c    221 g    284 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 6.1e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        225 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 267


RESULT 8
I08430
LOCUS       I08430                  1275 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 5 from Patent WO 8604606.
ACCESSION   I08430
VERSION     I08430.1  GI:588860
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1275)
  AUTHORS   Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
  TITLE     CYSTEINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
            NECROSIS FACTOR PROTEINS
  JOURNAL   Patent: WO 8604606-A 5 14-AUG-1986;
FEATURES             Location/Qualifiers
     source          1. .1275
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BASE COUNT      297 a    357 c    309 g    312 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 6e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db        697 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 739


RESULT 9
I07953
LOCUS       I07953                  1323 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 6 from Patent EP 0168214.
ACCESSION   I07953
VERSION     I07953.1  GI:589335
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1323)
  AUTHORS   Aggarwal,B.B., Lee,S.H., Goeddel,D.V. and Nedwin,G.E.
  TITLE     Tumor necrosis factor, methods for its preparation, compositions
            containing it, DNA encoding it and assay method using such DNA
  JOURNAL   Patent: EP 0168214-A2 6 15-JAN-1986;
FEATURES             Location/Qualifiers
     source          1. .1323
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BASE COUNT      298 a    387 c    308 g    330 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 6e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        754 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 796


RESULT 10
E00702
LOCUS       E00702                  1324 bp    RNA     linear   PAT 29-SEP-1997
DEFINITION  cDNA encoding human tumor necrosis factor.
ACCESSION   E00702
VERSION     E00702.1  GI:2168979
KEYWORDS    JP 1986040221-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1324)
  AUTHORS   Baraa,B.A., Debitsudo,B.G., San,H.R. and Guren,E.N.
  TITLE     TUMOR NECTROTIC FACTOR
  JOURNAL   Patent: JP 1986040221-A 1 26-FEB-1986;
            GENENTECH INC
COMMENT     OS   homosapiens
            PN   JP 1986040221-A/1
            PD   26-FEB-1986
            PF   05-JUL-1985 JP 1985149075
            PR   05-JUL-1984 US 84    627959, 05-JUL-1984 US 84    628059, PR
            05-JUL-1984 US 84    628060, 03-DEC-1984 US 84    677156, PR
            03-DEC-1984 US 84    677257, 03-DEC-1984 US 84    677454 PI   BARAA
            BUSHIYAN AGAAWARU, DEBITSUDO BANNOOMAN GETSUDERU, PI   SAN HII RII,
            PI   GUREN EBAN NEDOUIN
            PC   A61K35/12,A61K35/02,A61K35/14,A61K35/74,A61K37/04,C07H21/02,
            PC   C07H21/04,
            PC   C12N15/00;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            CC   *source: cell_type=promyelocytes;
            CC   *source: cell_line=HL-60;
            CC   *source: clone=lambda42-4, lambda16-4;
            FH   Key             Location/Qualifiers
            FH
            FT   sig_peptide     <1. .61
            FT   mat_peptide     62. .532
            FT                   /product='tumor necrosis factor' FT   CDS
              <1. .535
            FT                   /product='tumor necrosis factor' FT   3'UTR
              536. .>1324.
FEATURES             Location/Qualifiers
     source          1. .1324
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                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"
BASE COUNT      298 a    387 c    308 g    331 t
ORIGIN

  Query Match             100.0%;  Score 43;  DB 6;  Length 1324;
  Best Local Similarity   100.0%;  Pred. No. 6e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        755 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 797


RESULT 11
I03610
LOCUS       I03610                  1324 bp ss-DNA     linear   PAT 21-MAY-1993
DEFINITION  Sequence 2 from Patent US 4650674.
ACCESSION   I03610
VERSION     I03610.1  GI:268632
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 1324)
  AUTHORS   Aggarwal,B.B. and Lee,S.He.
  TITLE     Synergistic cytotoxic composition
  JOURNAL   Patent: US 4650674-A 2 17-MAR-1987;
            Genentech, Inc.; So. San Francisco, CA
FEATURES             Location/Qualifiers
     source          1. .1324
                     /organism="unknown"
BASE COUNT      298 a    387 c    308 g    331 t
ORIGIN

  Query Match           100.0%;  Score 43;  DB 6;  Length 1324;
  Best Local Similarity  100.0%;  Pred. No. 6e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        755 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 797


RESULT 12
SYNTNFTRP
LOCUS       SYNTNFTRP               1379 bp    mRNA    linear   SYN 27-APR-1993
DEFINITION  Synthetic human tumor necrosis factor mRNA, complete cds.
ACCESSION   M35592
VERSION     M35592.1  GI:209485
KEYWORDS    tumor necrosis factor.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1379)
  AUTHORS   Nobuhara,M., Kanamori,T., Nagase,Y., Nii,A., Morishita,H.,
            Tohyama,J., Andoh,S. and Kurimoto,M.
  TITLE     The expression of human tumor necrosis factor in E. coli
  JOURNAL   Nucleic Acids Symp. Ser. 17, 131-134 (1986)
  MEDLINE   87174864
   PUBMED   3031624
COMMENT     Original source text: Altered human leukemic B-cell line Ball-1,
            cDNA to mRNA, clone pM324-346.
FEATURES             Location/Qualifiers
     source          1. .1379
                     /organism="synthetic construct"
                     /mol_type="mRNA"
                     /db_xref="taxon:32630"
     CDS             178. .879
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     sig_peptide     178. .399
                     /note="synthetic tumor necrosis factor signal peptide"
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                     /product="synthetic tumor necrosis factor"
BASE COUNT      318 a    438 c    336 g    287 t
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  Best Local Similarity  100.0%;  Pred. No. 6e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db       1100 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1142


RESULT 13
I04244
LOCUS       I04244                  1465 bp ss-DNA     linear   PAT 21-MAY-1993
DEFINITION  Sequence 2 from Patent US 4677197.
ACCESSION   I04244
VERSION     I04244.1  GI:268725
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1465)
  AUTHORS   Lin,L.S. and Yamamoto,R.
  TITLE     Purification method for tumor necrosis factor
  JOURNAL   Patent: US 4677197-A 2 30-JUN-1987;
            Cetus Corporation; Emeryville, CA
FEATURES             Location/Qualifiers
     source          1. .1465
                     /organism="unknown"
BASE COUNT      324 a    429 c    363 g    349 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 6e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db        887 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 929


RESULT 14
I08863
LOCUS       I08863                  1560 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 3 from Patent WO 8806625.
ACCESSION   I08863
VERSION     I08863.1  GI:588416
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1560)
  AUTHORS   Mark,D.F., Lin,L.S., Thomsom,J.W. and Yamamoto,R.
  TITLE     ARGININE-DEPLETED HUMAN TUMOR NECROSIS FACTOR
  JOURNAL   Patent: WO 8806625-A 3 07-SEP-1988;
FEATURES             Location/Qualifiers
     source          1. .1560
                     /organism="unknown"
BASE COUNT      340 a    473 c    381 g    366 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 5.9e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db       1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049


RESULT 15
A37272
LOCUS       A37272                  1585 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 12 from Patent WO9404196.
ACCESSION   A37272
VERSION     A37272.1  GI:2294369
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1585)
  AUTHORS   Vile,R.G. and Hart,I.R.
  TITLE     TUMOUR THERAPY
  JOURNAL   Patent: WO 9404196-A 12 03-MAR-1994;
            IMP CANCER RES TECH (GB)
FEATURES             Location/Qualifiers
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     source          1. .1585
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
BASE COUNT      352 a     473 c     389 g     371 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.9e-07;
  Matches   43;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
              |||||||||||||||||||||||||||||||||||||||||||
Db       1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049


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GenCore version 5.1.6

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Perfect score: 104
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Searched: 2888711 seqs, 20454813386 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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37: em_htg_vrt:*
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39: em_htgo_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		104	100.0	400	11	G13533	G13533 SHGC-11076
2		104	100.0	787	6	AR300453	AR300453 Sequence
3		104	100.0	787	6	BD070551	BD070551 Self-regu
4		104	100.0	787	6	BD137681	BD137681 Self-regu
5		104	100.0	1275	6	I08430	I08430 Sequence 5
6		104	100.0	1323	6	I07953	I07953 Sequence 6
7		104	100.0	1324	6	E00702	E00702 cDNA encodi
8		104	100.0	1324	6	I03610	I03610 Sequence 2
9		104	100.0	1465	6	I04244	I04244 Sequence 2
10		104	100.0	1585	6	A37272	A37272 Sequence 12
11		104	100.0	1585	6	I04169	I04169 Sequence 1
12		104	100.0	1585	6	I04198	I04198 Sequence 1
13		104	100.0	1585	6	I08384	I08384 Sequence 5
14		104	100.0	1585	6	I08429	I08429 Sequence 3
15		104	100.0	1585	9	HUMTNFAA	M10988 Human tumor
16		104	100.0	1606	6	I07541	I07541 Sequence 22
17		104	100.0	1643	6	AR146199	AR146199 Sequence
18		104	100.0	1643	9	HSTNFR	X01394 Human mRNA
19		104	100.0	1676	9	BC028148	BC028148 Homo sapi
20		104	100.0	2270	6	AR300459	AR300459 Sequence
21		104	100.0	2270	6	BD137687	BD137687 Self-regu
22		104	100.0	2570	6	AR300460	AR300460 Sequence
23		104	100.0	2570	6	BD137688	BD137688 Self-regu
24		104	100.0	3103	9	HUMTNFX	M26331 Human tumor
25		104	100.0	3634	6	AR100270	AR100270 Sequence
26		104	100.0	3634	6	AR149925	AR149925 Sequence
27		104	100.0	3634	6	BD064008	BD064008 Novel exp
28		104	100.0	3634	9	HSTNFA	X02910 Human gene
29		104	100.0	4830	9	AY066019	AY066019 Homo sapi
30		104	100.0	6974	9	AB088112	AB088112 Homo sapi
31		104	100.0	7112	6	AX100950	AX100950 Sequence
32		104	100.0	7112	6	AX100965	AX100965 Sequence
33		104	100.0	7112	9	HUMTNFAB	M16441 Human tumor
34		104	100.0	7240	9	AY214167	AY214167 Homo sapi
35	c	104	100.0	16310	9	HSTNFABX	Z15026 Homo sapien
36		104	100.0	40160	9	BX248519	BX248519 Human DNA
37		104	100.0	61358	9	AL929587	AL929587 Human DNA
38	c	104	100.0	81800	9	HSY14768	Y14768 Homo sapien
39	c	104	100.0	100000	9	AP000505	AP000505 Homo sapi
40		104	100.0	132330	9	AL662801	AL662801 Human DNA
41		104	100.0	135784	9	AL662847	AL662847 Human DNA
42	c	104	100.0	184666	9	DJ201G24	AF129756 Homo sapi
43		104	100.0	212055	2	AP000899	AP000899 Homo sapi
44		102.4	98.5	817	6	A16444	A16444 Xho-PstI fr
45		102.4	98.5	817	6	E02109	E02109 DNA sequenc

ALIGNMENTS

RESULT 1
G13533
LOCUS G13533 400 bp DNA linear STS 30-MAR-2000
DEFINITION SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G13533
VERSION G13533.1 GI:1129272
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Olivier,M. and Cox,D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)

```
COMMENT
          Contact: Michael Olivier, David R. Cox
          Stanford Human Genome Center
          Stanford University School of Medicine
          4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
          Tel: (650) 320-5800
          Fax: (650) 320-5801
          Email: olivier@shgc.stanford.edu
          Primer A: CACTAAGAATTCAAACTGGGGC
          Primer B: GAGGAAGGCCTAAGGTCCAC
          STS size: 166
          PCR Profile:
                 Initial incubation: 94 degrees C for 90 seconds

                 Denaturation:       94 degrees C for 15 seconds
                 Annealing:          62 degrees C for 23 seconds
                 Polymerization:     72 degrees C for 30 seconds
                 PCR Cycles:         30
                 Thermal Cycler:     Perkin Elmer 9600
          Protocol:
                 Template:       25 ng
                 Primer:         each 1 uM
                 dNTPs:          each 200 uM
                 Taq Polymerase: 0.05 units/ul
                 Total Vol:      10 ul

          Buffer:
                 MgCl2:          2.5 mM
                 KCl:            50  mM
                 Tris-HCl:       20  mM
                 pH:             8.3

          Prepared with primer pairs derived from M10988 -- Unigene.
FEATURES             Location/Qualifiers
     source          1. .400
                     /organism="Homo sapiens"
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BASE COUNT      104 a    120 c     87 g     89 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 9.5e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
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RESULT 2
AR300453
LOCUS       AR300453                 787 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 7 from patent US 6537784.
ACCESSION   AR300453
VERSION     AR300453.1  GI:31687895
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 787)
  AUTHORS   Tatake,R.J., Marlin,S.D. and Barton,R.W.
  TITLE     Self-regulated apoptosis of inflammatory cells by gene therapy
  JOURNAL   Patent: US 6537784-A 7 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .787
                     /organism="unknown"
BASE COUNT      190 a    204 c    172 g    221 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 9.7e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 281

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        282 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 325


RESULT 3
BD070551
LOCUS       BD070551                 787 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Self-regulated apoptosis of inflammatory cells by gene therapy.
ACCESSION   BD070551
VERSION     BD070551.1  GI:22616154
KEYWORDS    JP 2001516210-A/13.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 787)
  AUTHORS   Tatake,R.J., Marlin,S.D. and Barton,R.W.
  TITLE     Self-regulated apoptosis of inflammatory cells by gene therapy
  JOURNAL   Patent: JP 2001516210-A 13 25-SEP-2001;
            BOEHRINGER INGELHEIM PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2001516210-A/13
            PD   25-SEP-2001
            PF   27-FEB-1998 JP 1998537909
            PR   28-FEB-1997 US    60/039266
            PI   REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC
            A61K31/70,C07H21/04,C12N15/12,C12P19/34
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   TNF alpha nontranslated region
            FH   Key             Location/Qualifiers
            FT   source          1. .787
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .787
                     /organism="unidentified"
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BASE COUNT      190 a    204 c    172 g    221 t
ORIGIN

  Query Match             100.0%;  Score 104;  DB 6;  Length 787;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 281

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        282 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 325


RESULT 4
BD137681
LOCUS       BD137681                 787 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Self-regulated apoptosis of inflammatory cells by gene therapy.
ACCESSION   BD137681
```

```
VERSION     BD137681.1  GI:23232626
KEYWORDS    JP 2002504381-A/7.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 787)
  AUTHORS   Tatake,R.J., Marlin,S.D. and Barton,R.W.
  TITLE     Self-regulated apoptosis of inflammatory cells by gene therapy
  JOURNAL   Patent: JP 2002504381-A 7 12-FEB-2002;
            BOEHRINGER INGELHEIM PHARMACEUTICALS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002504381-A/7
            PD   12-FEB-2002
            PF   12-JAN-1999 JP 2000533579
            PR   27-FEB-1998 US    60/076316
            PI   REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC
            C12N15/09,A61K31/7088,A61K48/00,A61P1/04,A61P3/10,A61P17/06, PC
            A61P25/00,
            PC   A61P29/00,A61P43/00,C12N9/64,C12Q1/68//C12N5/10,C12N15/00, PC
             C12N5/00
            CC   TNF-alpha untranslated region
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .787
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ORIGIN

  Query Match           100.0%;  Score 104;  DB 6;  Length 787;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        282 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 325


RESULT 5
I08430
LOCUS       I08430                  1275 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 5 from Patent WO 8604606.
ACCESSION   I08430
VERSION     I08430.1  GI:588860
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1275)
  AUTHORS   Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
  TITLE     CYSTEINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
            NECROSIS FACTOR PROTEINS
  JOURNAL   Patent: WO 8604606-A 5 14-AUG-1986;
FEATURES             Location/Qualifiers
     source          1. .1275
                     /organism="unknown"
BASE COUNT      297 a    357 c    309 g    312 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 9.9e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        693 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 752

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        753 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 796


RESULT 6
I07953
LOCUS       I07953                  1323 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 6 from Patent EP 0168214.
ACCESSION   I07953
VERSION     I07953.1  GI:589335
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1323)
  AUTHORS   Aggarwal,B.B., Lee,S.H., Goeddel,D.V. and Nedwin,G.E.
  TITLE     Tumor necrosis factor, methods for its preparation, compositions
            containing it, DNA encoding it and assay method using such DNA
  JOURNAL   Patent: EP 0168214-A2 6 15-JAN-1986;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      298 a    387 c    308 g    330 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 9.9e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        750 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 809

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        810 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 853


RESULT 7
E00702
LOCUS       E00702                  1324 bp    RNA     linear   PAT 29-SEP-1997
DEFINITION  cDNA encoding human tumor necrosis factor.
ACCESSION   E00702
VERSION     E00702.1  GI:2168979
KEYWORDS    JP 1986040221-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1324)
  AUTHORS   Baraa,B.A., Debitsudo,B.G., San,H.R. and Guren,E.N.
  TITLE     TUMOR NECTROTIC FACTOR
  JOURNAL   Patent: JP 1986040221-A 1 26-FEB-1986;
            GENENTECH INC
COMMENT     OS   homosapiens
            PN   JP 1986040221-A/1
            PD   26-FEB-1986
            PF   05-JUL-1985 JP 1985149075
            PR   05-JUL-1984 US 84    627959, 05-JUL-1984 US 84    628059, PR
            05-JUL-1984 US 84    628060, 03-DEC-1984 US 84    677156, PR
            03-DEC-1984 US 84    677257, 03-DEC-1984 US 84    677454 PI   BARAA
            BUSHIYAN AGAAWARU, DEBITSUDO BANNOOMAN GETSUDERU, PI   SAN HII RII,
            PI   GUREN EBAN NEDOUIN
            PC   A61K35/12,A61K35/02,A61K35/14,A61K35/74,A61K37/04,C07H21/02,
            PC   C07H21/04,
            PC   C12N15/00;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
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          CC   *source: cell_type=promyelocytes;
          CC   *source: cell_line=HL-60;
          CC   *source: clone=lambda42-4, lambda16-4;
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          FH
          FT   sig_peptide     <1. .61
          FT   mat_peptide     62. .532
          FT                   /product='tumor necrosis factor' FT   CDS
            <1. .535
          FT                   /product='tumor necrosis factor' FT   3'UTR
            536. .>1324.
FEATURES             Location/Qualifiers
     source          1. .1324
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                     /mol_type="genomic RNA"
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BASE COUNT      298 a    387 c    308 g    331 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 9.9e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
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Db        811 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 854


RESULT 8
I03610
LOCUS       I03610                1324 bp ss-DNA     linear   PAT 21-MAY-1993
DEFINITION  Sequence 2 from Patent US 4650674.
ACCESSION   I03610
VERSION     I03610.1  GI:268632
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1324)
  AUTHORS   Aggarwal,B.B. and Lee,S.He.
  TITLE     Synergistic cytotoxic composition
  JOURNAL   Patent: US 4650674-A 2 17-MAR-1987;
            Genentech, Inc.; So. San Francisco, CA
FEATURES             Location/Qualifiers
     source          1. .1324
                     /organism="unknown"
BASE COUNT      298 a    387 c    308 g    331 t
ORIGIN

  Query Match           100.0%;  Score 104;  DB 6;  Length 1324;
  Best Local Similarity  100.0%;  Pred. No. 9.9e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        811 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 854


RESULT 9
I04244
LOCUS       I04244                1465 bp ss-DNA     linear   PAT 21-MAY-1993
DEFINITION  Sequence 2 from Patent US 4677197.
ACCESSION   I04244
VERSION     I04244.1  GI:268725
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1465)
  AUTHORS   Lin,L.S. and Yamamoto,R.
  TITLE     Purification method for tumor necrosis factor
  JOURNAL   Patent: US 4677197-A 2 30-JUN-1987;
            Cetus Corporation; Emeryville, CA
FEATURES             Location/Qualifiers
     source          1. .1465
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BASE COUNT      324 a    429 c    363 g    349 t
ORIGIN

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        883 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 942

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        943 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 986


RESULT 10
A37272
LOCUS       A37272                1585 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 12 from Patent WO9404196.
ACCESSION   A37272
VERSION     A37272.1  GI:2294369
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1585)
  AUTHORS   Vile,R.G. and Hart,I.R.
  TITLE     TUMOUR THERAPY
  JOURNAL   Patent: WO 9404196-A 12 03-MAR-1994;
            IMP CANCER RES TECH (GB)
FEATURES             Location/Qualifiers
     source          1. .1585
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BASE COUNT      352 a    473 c    389 g    371 t
ORIGIN

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Db       1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
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Db       1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1106


RESULT 11
I04169
LOCUS       I04169                1585 bp ss-DNA     linear   PAT 21-MAY-1993
DEFINITION  Sequence 1 from Patent US 4677063.
ACCESSION   I04169
VERSION     I04169.1  GI:268716
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 1585)
  AUTHORS   Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van
            Arsdell,J.
  TITLE     Human tumor necrosis factor
  JOURNAL   Patent: US 4677063-A 1 30-JUN-1987;
            Cetus Corporation; Emeryville, CA
FEATURES             Location/Qualifiers
     source          1. .1585
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BASE COUNT      352 a    473 c    389 g    371 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1e-24;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Db       1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1106


RESULT 12
I04198
LOCUS       I04198                  1585 bp ss-DNA     linear   PAT 21-MAY-1993
DEFINITION  Sequence 1 from Patent US 4677064.
ACCESSION   I04198
VERSION     I04198.1  GI:268719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1585)
  AUTHORS   Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Van Arsdell,J.N.
            and Lin,L.S.
  TITLE     Human tumor necrosis factor
  JOURNAL   Patent: US 4677064-A 1 30-JUN-1987;
            Cetus Corporation; Emeryville, CA
FEATURES             Location/Qualifiers
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BASE COUNT      352 a    473 c    389 g    371 t
ORIGIN

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Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Db       1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1106


RESULT 13
I08384
LOCUS       I08384                  1585 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 5 from Patent WO 8602381.
ACCESSION   I08384
VERSION     I08384.1  GI:588904
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1585)
  AUTHORS   Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van
            Arsdell,J.N.
  TITLE     HUMAN TUMOR NECROSIS FACTOR
  JOURNAL   Patent: WO 8602381-A 5 24-APR-1986;
FEATURES             Location/Qualifiers
     source          1. .1585
                     /organism="unknown"
BASE COUNT      352 a    473 c    389 g    371 t
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Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
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Db       1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1106


RESULT 14
I08429
LOCUS       I08429                  1585 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 3 from Patent WO 8604606.
ACCESSION   I08429
VERSION     I08429.1  GI:588859
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1585)
  AUTHORS   Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
  TITLE     CYSTEINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
            NECROSIS FACTOR PROTEINS
  JOURNAL   Patent: WO 8604606-A 3 14-AUG-1986;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      352 a    473 c    389 g    371 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1e-24;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1106


RESULT 15
HUMTNFAA
LOCUS       HUMTNFAA                1585 bp    mRNA    linear   PRI 14-JAN-1995
DEFINITION  Human tumor necrosis factor (TNF) mRNA.
ACCESSION   M10988
VERSION     M10988.1  GI:339737
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1585)
  AUTHORS   Wang,A.M., Creasey,A.A., Ladner,M.B., Lin,L.S., Strickler,J., Van
            Arsdell,J.N., Yamamoto,R. and Mark,D.F.
  TITLE     Molecular cloning of the complementary DNA for human tumor necrosis
            factor
  JOURNAL   Science 228 (4696), 149-154 (1985)
  MEDLINE   85142190
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   PUBMED   3856324
COMMENT     Original source text: Human cDNA to mRNA, clone pE4.
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                     /db_xref="taxon:9606"
                     /map="6p21.3"
     gene            1. .1585
                     /gene="TNFA"
     CDS             86. .787
                     /gene="TNFA"
                     /note="tumor necrosis factor"
                     /codon_start=1
                     /protein_id="AAA61198.1"
                     /db_xref="GI:339738"
                     /db_xref="GDB:G00-120-441"
                     /translation="MSTESMIRDVELAEEALPKKTGGPQGSRRCLFLSLFSFLIVAGA
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                     VSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYL
                     DFAESGQVYFGIIAL"
BASE COUNT      352 a    473 c    389 g    371 t
ORIGIN      Chromosome 6p21.3.

  Query Match            100.0%;  Score 104;  DB 9;  Length 1585;
  Best Local Similarity  100.0%;  Pred. No. 1e-24;
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Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Db       1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
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Db       1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1106


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Job time : 1094.23 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 3, 2004, 03:10:21 ; Search time 287.946 Seconds
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Title: US-09-801-371A-1
Perfect score: 104
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	104	100.0	104	21	AAZ99816	Cis-acting nucleot
2	104	100.0	787	20	AAZ20979	Human TNFalpha 3'U
3	104	100.0	1275	7	AAN60558	Sequence encoding
4	104	100.0	1323	7	AAN60363	Sequence encoding
5	104	100.0	1324	21	AAF21085	Human low adenosin
6	104	100.0	1324	21	AAA34963	Human adenosine re
7	104	100.0	1560	9	AAN80219	Sequence of pE4 en
8	104	100.0	1585	7	AAN60557	Sequence encoding
9	104	100.0	1606	7	AAN60446	Sequence encoding
10	104	100.0	1606	17	AAT15424	Human tumour necro
11	104	100.0	1643	17	AAT31021	Human tumour necro
12	104	100.0	1643	24	ABK13195	Human tumour necro
13	104	100.0	1643	25	AAD49644	Human tumour necro
14	104	100.0	1643	25	AAL53712	Tumour necrosis fa
15	104	100.0	2270	20	AAZ20983	Chimeric nucleic a
16	104	100.0	2570	20	AAZ20984	Chimeric nucleic a
17	104	100.0	3634	19	AAV39005	TNF-alpha gene use
18	104	100.0	3634	20	AAX09014	Tumour necrosis fa
19	104	100.0	3634	21	AAC63770	Human TNF-alpha ge
20	104	100.0	3634	21	AAA40760	Human tumour necro
21	104	100.0	6911	24	AAD45858	Human tumour necro
22	104	100.0	6911	24	AAD45898	Human tumour necro
23	104	100.0	7112	22	AAF86085	Lymphotoxin and tu
24	104	100.0	7112	22	AAF57450	Human tumour necro
25	104	100.0	7112	25	AAL51863	Human tumour necro
c 26	104	100.0	16310	21	AAF21086	Human low adenosin
c 27	104	100.0	16310	21	AAA34964	Human adenosine re
28	104	100.0	17634	21	AAF21087	Human low adenosin
c 29	104	100.0	17634	21	AAF21087	Human low adenosin
30	104	100.0	17634	21	AAA34965	Human adenosine re
c 31	104	100.0	17634	21	AAA34965	Human adenosine re
c 32	104	100.0	81800	24	ABK84756	Human cDNA differe
33	102.4	98.5	817	11	AAQ04340	THP-1. Homo sapie
34	102.4	98.5	818	10	AAN91035	XhoI - PstI sectio
35	102.4	98.5	1200	8	AAN70072	Human anti-tumor p
36	102.4	98.5	1200	10	AAN90969	Part of gene for a
37	102.4	98.5	1585	7	AAN60527	Sequence encoding
38	102.4	98.5	1585	15	AAQ58037	Tumor necrosis fac
39	102.4	98.5	1643	8	AAN71307	Sequence encoding
40	91.8	88.3	815	8	AAN70075	Human anti-tumor p
41	50	48.1	50	21	AAZ99815	Sequence of the st
42	43	41.3	43	21	AAZ99817	Cis-acting nucleot
43	33	31.7	51	21	AAZ99916	Sequence of the st
44	31.4	30.2	10240	19	AAV39007	Porcine TNF-alpha
45	30.2	29.0	2980	22	AAK86235	Human immune/haema

ALIGNMENTS

RESULT 1
AAZ99816
ID AAZ99816 standard; RNA; 104 BP.
XX
AC AAZ99816;
XX
DT 12-JUL-2000 (first entry)
XX
DE Cis-acting nucleotide sequence derived from human TNF-alpha.
XX
KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200014255-A1.
XX
PD 16-MAR-2000.
XX
PF 06-SEP-1999; 99WO-IL00483.
XX
PR 07-SEP-1998; 98IL-0126112.
PR 26-OCT-1998; 98IL-0126757.
XX
PA (YISS) YISSUM RES & DEV CO.
XX
PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
XX
DR WPI; 2000-257000/22.
XX

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PT   Regulation of gene expression by mRNA splicing is carried out using a
PT   cis-acting nucleotide sequence controlled by phosphorylation of the
PT   alpha-subunit of eukaryotic initiation factor 2  -
XX
PS   Claim 4; Page 15; 75pp; English.
XX
CC   The specification describes a cis-acting nucleotide sequence which is
CC   capable of removing introns from a precursor transcript encoded by a
CC   gene which harbours at least one cis-acting nucleotide sequence. This
CC   removal is effected during the production of mRNA of the gene, and
CC   depends on activation of a trans-acting factor which is an RNA-activated
CC   protein kinase capable of phosphorylating the alpha-subunit of eukaryotic
CC   initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
CC   sequence, derived from the 3' untranslated region (3'UTR) of the human
CC   tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
CC   splicing of precursor transcripts encoded by that gene sensitive to the
CC   level of RNA-activated protein kinase (PKR) activity. The sequence can
CC   be used to transform host cells to regulate gene expression at the mRNA
CC   splicing level, for gene therapy, and to produce a recombinant
CC   therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC   protein) or industrially or agriculturally applicable protein. The
CC   present sequence represents a cis-acting nucleotide sequence of the
CC   invention.
XX
SQ   Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 other;

  Query Match             100.0%;  Score 104;  DB 21;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104


RESULT 2
AAZ20979
ID   AAZ20979 standard; DNA; 787 BP.
XX
AC   AAZ20979;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human TNFalpha 3'UTR.
XX
KW   TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW   chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW   psoriasis; graft versus host disease; lupus erythematosus;
KW   diabetes; ankylosing spondylitis; rheumatoid arthritis; ds.
XX
OS   Homo sapiens.
XX
PN   WO9943840-A1.
XX
PD   02-SEP-1999.
XX
PF   12-JAN-1999;   99WO-US00637.
XX
PR   27-FEB-1998;   98US-0076316.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX
PI   Tatake RJ,  Marlin SD,  Barton RW;
XX
DR   WPI; 1999-527630/44.
XX
PT   A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)
PT   promoter and an apoptosis-inducing Granzyme B polynucleotide  -
XX
PS   Example 1; Page 60-61; 71pp; English.
XX
CC   This sequence represents a human TNFalpha (tumour necrosis factor alpha)
CC   3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984)
CC   were constructed comprising at least one TNFalpha promoter enhancer
CC   region (AAZ20975-Z20978), a TNFalpha promoter (AAZ20972-Z20974), a DNA
CC   encoding the apoptosis-inducing Granzyme B protein (AAZ20982), and a
CC   TNFalpha 3'UTR sequence. TNFalpha is one of a number of
CC   cytokines produced by inflammatory  cells. Upregulation and/or
CC   dysregulation of cytokines in inflamed tissue may be directly or
CC   indirectly responsible for exacerbation of chronic inflammatory
CC   diseases. Introduction of the chimeric nucleotide to activated
CC   inflammatory cells causes them to undergo apoptosis. Pharmaceutical
CC   compositions of the chimeric nucleotide may be useful for treating
CC   inflammatory disorders such as multiple sclerosis, Crohn's disease,
CC   ulcerative colitis, psoriasis, graft versus host disease, lupus
CC   erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing
CC   spondylitis, and in particular, rheumatoid arthritis. The use of such
CC   chimeric nucleotides offers simpler and cheaper long-term relief, in
CC   comparison with existing conventional pharmaceutical and invasive surgery
CC   methods.
XX
SQ   Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 other;

  Query Match             100.0%;  Score 104;  DB 20;  Length 787;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 281

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 325


RESULT 3
AAN60558
ID   AAN60558 standard; DNA; 1275 BP.
XX
AC   AAN60558;
XX
DT   28-JUL-1991  (first entry)
XX
DE   Sequence encoding mature human tumour necrosis factor (hTNF) mutein
DE   Ser 69 in pAW731.
XX
KW   Antitumour; anticancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..474
FT                   /*tag=  a
XX
PN   WO8604606-A.
XX
PD   14-AUG-1986.
XX
PF   03-FEB-1986;   86WO-US00236.
XX
PR   07-FEB-1985;   85US-0698939.
PR   19-OCT-1982;   82US-0435154.
PR   15-APR-1983;   83US-0486162.
PR   20-DEC-1983;   83US-0564224.
PR   15-OCT-1984;   84US-0661026.
PR   07-FEB-1985;   85US-0695934.
XX
PA   (CETU ) CETUS CORP.
XX
PI   Mark DF,  Lin LS,  Lu SDY,  Wang AM;
XX
```

```
DR   WPI; 1986-225458/34.
DR   P-PSDB; AAP60656.
XX
PT   New synthetic muteins of human tumour necrosis factor protein -
PT   are obtd. by direct mutagenesis and retain antitumour activity
XX
PS   Disclosure; Fig 3a; 47pp; English.
XX
CC   The sequence encoding TNF produced by the promyelocytic leukemia
CC   cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in
CC   E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in
CC   the TNF sequence appears to be involved in disulphide linkages. The
CC   patentors claim a novel synthetic mutein of a biologically active
CC   hTNF protein, having at least one cysteine residue free from a
CC   disulphide link and non-essential to the activity and having at
CC   least one of the cysteine residues deleted or replaced by another AA.
CC   Plasmid pAW731 (Ser 69) is claimed.
XX
SQ   Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 other;

  Query Match             100.0%;  Score 104;  DB 7;  Length 1275;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 752

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        753 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 796


RESULT 4
AAN60363
ID   AAN60363 standard; DNA; 1323 BP.
XX
AC   AAN60363;
XX
DT   19-JUN-1991  (first entry)
XX
DE   Sequence encoding human tumour necrosis factor.
XX
KW   hTNF; tumour; cancer; interferon; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..534
FT                   /*tag=  a
FT   sig_peptide     1..60
FT                   /*tag=  b
FT                   /label= Secretory leader peptide
FT   mat_peptide     61..534
FT                   /*tag=  c
XX
PN   EP168214-A.
XX
PD   15-JAN-1986.
XX
PF   03-JUL-1985;   85EP-0304758.
XX
PR   03-DEC-1984;   84US-0677454.
PR   05-JUL-1984;   84US-0627959.
PR   05-JUL-1984;   84US-0628059.
PR   05-JUL-1984;   84US-0628060.
PR   03-DEC-1984;   84US-0677156.
PR   03-DEC-1984;   84US-0677257.
PR   25-JUL-1984;   84US-0627969.
PR   03-DEC-1984;   84US-0677267.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Aggarwal BB,  Lee SH,  Goeddel DV,  Nedwin GE;
XX
DR   WPI; 1986-015483/03.
DR   P-PSDB; AAP60417.
XX
PT   Pure tumour necrosis factor and mutant forms - new DNA coding
PT   sequences and transformed cells.
XX
PS   Claim 20; Fig 10; 90pp; English.
XX
CC   Sequence encodes the pure human tumour necrosis factor, mutants of
CC   which are covered by the claims. TNF and mutants are useful in
CC   treating tumours, especially in tandem with interferon. The
CC   encoding sequence may be used to create plasmid pTrpXAPTNF, allowing
CC   transformation of an E.coli host for the expression of TNF.
XX
SQ   Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 other;

  Query Match             100.0%;  Score 104;  DB 7;  Length 1323;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 809

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db        810 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 853


RESULT 5
AAF21085
ID   AAF21085 standard; DNA; 1324 BP.
XX
AC   AAF21085;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Human low adenosine antisense oligonucleotide related sequence #2652.
XX
KW   Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW   human; airway disorder; bronchoconstriction; lung inflammation;
KW   surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW   immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW   respiratory obstruction; pulmonary obstruction; impeded respiration;
KW   surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW   respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW   pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW   chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW   cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200062736-A2.
XX
PD   26-OCT-2000.
XX
PF   24-MAR-2000; 2000WO-US08020.
XX
PR   06-APR-1999;   99US-0127958.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
PA   (NYCE/) NYCE J W.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-679539/66.
XX
PT   Low adenosine (A) content antisense oligonucleotides which do not
PT   trigger adenosine receptors during metabolism, useful e.g. for treating
PT   cancers and respiratory obstructions -
XX
```

PS Disclosure; Page 887; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;

Query Match 100.0%; Score 104; DB 21; Length 1324;
Best Local Similarity 100.0%; Pred. No. 2.7e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 751 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810

Qy 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
Db 811 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 854

RESULT 6
AAA34963
ID AAA34963 standard; DNA; 1324 BP.
XX
AC AAA34963;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2652.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US17712.
XX
PR 03-AUG-1998; 98US-0095212.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
PS Disclosure; Page 814-815; 1343pp; English.
XX
CC The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 other;

Query Match 100.0%; Score 104; DB 21; Length 1324;
Best Local Similarity 100.0%; Pred. No. 2.7e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 751 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810

Qy 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
Db 811 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 854

RESULT 7
AAN80219
ID AAN80219 standard; DNA; 1560 BP.
XX
AC AAN80219;
XX
DT 28-DEC-1990 (first entry)
XX
DE Sequence of pE4 encoding human tumour necrosis factor (TNF).
XX
KW Lymphokine; antitumour; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 86..313

```
FT                   /*tag=  a
FT   mat_peptide     314..787
FT                   /*tag=  b
XX
PN   WO8806625-A.
XX
PD   07-SEP-1988.
XX
PF   25-JAN-1988;   88WO-US00183.
XX
PR   26-FEB-1987;   87US-0019221..
XX
PA   (CETU ) CETUS CORP.
XX
PI   Mark DF,  Thomson JW,  Lin LS,  Yamamoto R;
XX
DR   WPI; 1988-271165/38.
DR   P-PSDB; AAP80728.
XX
PT   Human tumour necrosis factor muteins -
PT   having comparable biological activity with improved stability
PT   and ease of purification
XX
PS   Disclosure; Fig 1-1 to 1-2; 51pp; English.
XX
CC   A human TNF protein which is modified from the sequence shown in
CC   AAP80728, including naturally ocurring allelic variants is claimed. Also
CC   claimed are: recombinant DNA sequences encoding the protein (AAN80219)
CC   and control sequences for expression; a vector; a transformed host cell;
CC   a method of producing the protein by culturing the host cell;
CC   pharmaceutical compsn. of the protein and a carrier and a method of
CC   treating tumour burden with the compsn. The muteins are capable of the
CC   range of biological activities exhibited by native TNF but exhibit
CC   improved stability and ease of purification.
XX
SQ   Sequence 1560 BP; 340 A; 473 C; 381 G; 366 T; 0 other;

  Query Match             100.0%;  Score 104;  DB 9;  Length 1560;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1106


RESULT 8
AAN60557
ID   AAN60557 standard; DNA; 1585 BP.
XX
AC   AAN60557;
XX
DT   28-JUL-1991  (first entry)
XX
DE   Sequence encoding mature human tumour necrosis factor (hTNF) in pE4.
XX
KW   Antitumour; anticancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             86..313
FT                   /*tag=  a
FT   mat_peptide     314..787
FT                   /*tag=  b
XX
PN   WO8604606-A.
XX
PD   14-AUG-1986.
XX
PF   03-FEB-1986;   86WO-US00236.
XX
PR   07-FEB-1985;   85US-0698939.
PR   19-OCT-1982;   82US-0435154.
PR   15-APR-1983;   83US-0486162.
PR   20-DEC-1983;   83US-0564224.
PR   15-OCT-1984;   84US-0661026.
PR   07-FEB-1985;   85US-0695934.
XX
PA   (CETU ) CETUS CORP.
XX
PI   Mark DF,  Lin LS,  Lu SDY,  Wang AM;
XX
DR   WPI; 1986-225458/34.
DR   P-PSDB; AAP60655.
XX
PT   New synthetic muteins of human tumour necrosis factor protein -
PT   are obtd. by direct mutagenesis and retain antitumour activity
XX
PS   Disclosure; Fig 1; 47pp; English.
XX
CC   The sequence encoding TNF produced by the promyelocytic leukemia
CC   cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in
CC   E.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in
CC   the TNF sequence appears to be involved in disulphide linkages. The
CC   patentors claim a novel synthetic mutein of a biologically active
CC   hTNF protein, having at least one cysteine residue free from a
CC   disulphide link and non-essential to the activity and having at
CC   least one of the cysteine residues deleted or replaced by another AA.
CC   Plasmid pAW731 (Ser 69) is claimed.
XX
SQ   Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 other;

  Query Match             100.0%;  Score 104;  DB 7;  Length 1585;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1106


RESULT 9
AAN60446
ID   AAN60446 standard; cDNA; 1606 BP.
XX
AC   AAN60446;
XX
DT   25-MAR-2003  (updated)
DT   07-AUG-1991  (first entry)
XX
DE   Sequence encoding tumour necrosis factor (TNF).
XX
KW   Anticancer agent; antitumour; antimalarial; tumour necrosis factor;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             158..859
FT                   /*tag=  a
XX
PN   WO8603751-A.
XX
PD   03-JUL-1986.
XX
PF   19-DEC-1985;   85WO-EP00721.
XX
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PR   09-OCT-1985;   85US-0785847.
PR   21-DEC-1984;   84US-0684595.
PR   09-OCT-1986;   86WO-US02133.
XX
PA   (BIOJ ) BIOGEN NV.
PA   (FIER/) FIERS W C.
PA   (ALLE/) ALLET B.
PA   (BIOJ ) BIOGEN INC.
XX
PI   Fiers WC,  Fransen LM,  Tavernier JHL,  Marmenout ALM;
PI   VanDerHeyden J,  Allet B,  Washima EH;
XX
DR   WPI; 1986-182891/28.
DR   P-PSDB; AAP60531.
XX
PT   Mammalian tumour necrosis factors - produced by culturing
PT   pro-karyotic hosts transformed with recombinant DNA
XX
PS   Example; Fig 9; 93pp; English.
XX
CC   TNF-like polypeptides and compsns. are produced by the fermentation
CC   of host cells transformed with at least one DNA sequence which codes
CC   for a mammalian TNF-like polypeptide operatively linked to an
CC   expression control sequence in the transformed host.
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 1606 BP; 357 A; 494 C; 394 G; 361 T; 0 other;

  Query Match             100.0%;  Score 104;  DB 7;  Length 1606;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1075 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1134

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1135 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1178


RESULT 10
AAT15424
ID   AAT15424 standard; cDNA; 1606 BP.
XX
AC   AAT15424;
XX
DT   25-MAR-2003  (updated)
DT   23-APR-1996  (first entry)
XX
DE   Human tumour necrosis factor cDNA clone p-hTNF-1.
XX
KW   Tumour necrosis factor; TNF; phage T4; phage lambda; pL promoter;
KW   antitumour; anticancer; antimalarial; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             158..859
FT                   /*tag=  a
FT   sig_peptide     158..385
FT                   /*tag=  b
FT   mat_peptide     386..856
FT                   /*tag=  c
XX
PN   US5487984-A.
XX
PD   30-JAN-1996.
XX
PF   20-DEC-1985;   85US-0811654.
XX
PR   20-DEC-1985;   85US-0811654.
PR   21-DEC-1984;   84US-0684595.
PR   09-OCT-1985;   85US-0785847.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Allet B,  Kawashima EH;
XX
DR   WPI; 1996-105230/11.
DR   P-PSDB; AAR88590.
XX
PT   Prodn. of tumour necrosis factor - using recombinant DNA encoding
PT   TNF under the control of T4 or lambda pL-T4 expression control
PT   sequences.
XX
PS   Example 9; Fig 9; 43pp; English.
XX
CC   A cDNA clone (AAT15424), p-hTNF-1 (DSM 3160), codes for the human
CC   tumour necrosis factor (hTNF) precursor (AAR88590).  It was obtd.
CC   by screening a human cDNA library with a fragment of mouse TNF
CC   cDNA.  The isolated cDNA may be linked to expression control
CC   sequences from phage T4 or phage lambda (see AAT15402-05 and
CC   AAT15425-26) for expression in host cells, esp. Escherichia coli,
CC   and commercial-scale prodn. of recombinant TNF of use as an
CC   antitumour, anticancer and antimalarial agent.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 1606 BP; 357 A; 494 C; 394 G; 361 T; 0 other;

  Query Match             100.0%;  Score 104;  DB 17;  Length 1606;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1075 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1134

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1135 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1178


RESULT 11
AAT31021
ID   AAT31021 standard; DNA; 1643 BP.
XX
AC   AAT31021;
XX
DT   26-SEP-1996  (first entry)
XX
DE   Human tumour necrosis factor cDNA clone HSTNFR.
XX
KW   Gene therapy; hypoxia related enhancer element; HREE; ischaemia;
KW   reperfusion; promoter; tumour necrosis factor; TNF; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             153..854
FT                   /*tag=  a
XX
PN   WO9620276-A1.
XX
PD   04-JUL-1996.
XX
PF   13-NOV-1995;   95WO-IB00996.
XX
PR   23-DEC-1994;   94US-0365486.
XX
PA   (STRI ) SRI INT.
XX
PI   Bishopric NH,  Green CJ,  Laderoute KR,  Murphy B;
PI   Webster KA;
XX
DR   WPI; 1996-321849/32.
```

```
DR   P-PSDB; AAW00454.
XX
PT   Chimeric gene contg. therapeutic gene linked to HREE - partic. for
PT   expressing SOD etc. in hypoxic tissue to reduce tissue injury caused
PT   by ischaemia or reperfusion
XX
PS   Example 8; Page 100-101; 118pp; English.
XX
CC   A PCR-generated DNA fragment (AAT31021) encoding human tumour
CC   necrosis factor (hTNF) (AAW00454). hTNF induces apoptosis and
CC   is not known to be induced by hypoxic stress. A -90 bp human
CC   metallothionein IIA promoter fragment (see also AAT31003) was
CC   inserted upstream of the hTNF gene and the construct was used
CC   to transfect mouse C2C12 myoblasts and A431 cells. Hypoxia-
CC   mediated TNF induction and tumour control were demonstrated
CC   in an animal xenograft model.
XX
SQ   Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 other;

  Query Match             100.0%;  Score 104;  DB 17;  Length 1643;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db       1130 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1173


RESULT 12
ABK13195
ID   ABK13195 standard; DNA; 1643 BP.
XX
AC   ABK13195;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human tumour necrosis factor alpha (TNF alpha) DNA.
XX
KW   TNF; apoptosis; ds; tumour; death domain receptor ligand;
KW   diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1;
KW   carcinoma; mammary adenocarcinoma; non-small cell lung carcinoma;
KW   neurological malignancy; haematological malignancy; lichen planus;
KW   non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;
KW   malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;
KW   non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;
KW   T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;
KW   discoid lupus erythematosus; human; gene; tumour necrosis factor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             153..854
FT                   /*tag= a
FT                   /product= "TNF alpha protein"
XX
PN   US6329148-B1.
XX
PD   11-DEC-2001.
XX
PF   15-FEB-2000; 2000US-0505250.
XX
PR   16-FEB-1999;   99US-120313P.
PR   20-AUG-1999;   99US-149989P.
XX
PA   (STRD ) UNIV LELAND STANFORD.
XX
PI   Rosen GD,  Kao P;
XX
DR   WPI; 2002-121125/16.
DR   P-PSDB; AAU75065.
XX
PT   Use of a synergistic combination of death domain receptor ligands and
PT   diterpenoid triepoxides for killing of tumour cells -
XX
PS   Disclosure; Column 27-30; 20pp; English.
XX
CC   This invention relates to a novel method for enhanced killing of tumour
CC   cells comprising contacting a tumour cell with a synergistic
CC   combination of a death domain receptor ligand and a diterpenoid
CC   triepoxide. This method has cytostatic activity and works by blocking
CC   TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the
CC   invention may be used for treating tumours, particularly solid tumours,
CC   e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma
CC   also neurological malignancies, haematological malignancies, e.g.
CC   non-Hodgkin's lymphoma, chronic lymphocytic leukaemia, malignant
CC   cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma,
CC   lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia,
CC   bullous pemphigoid, discoid lupus erythematosus, lichen planus. The
CC   combination may be administered with other active agents, e.g. anti-
CC   metastatic, anti-tumour or anti-angiogenic agents. The potent synergy
CC   between the diterpenoids and the death domain ligands allows increased
CC   killing at equivalent or lower doses, and can sensitise otherwise
CC   resistant cells. This sequence represents the human tumour necrosis
CC   factor alpha (TNF alpha) DNA. TNF alpha is a ligand for death
CC   domain receptors used in the used method of the invention in
CC   combination with diterpenoid triepoxides to kill tumours by
CC   induction of apoptosis.
XX
SQ   Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 other;

  Query Match             100.0%;  Score 104;  DB 24;  Length 1643;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db       1130 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1173


RESULT 13
AAD49644
ID   AAD49644 standard; DNA; 1643 BP.
XX
AC   AAD49644;
XX
DT   24-MAR-2003  (first entry)
XX
DE   Human tumour necrosis factor alpha (TNF-alpha) DNA.
XX
KW   Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;
KW   gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis;
KW   autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic;
KW   neurodegenerative disorder; Parkinson's disease; gene therapy; virucide;
KW   haemostatic; antibacterial; nootropic; neuroprotective; cytostatic;
KW   fungicide; human; tumour necrosis factor alpha; TNF-alpha; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..152
FT                   /*tag= a
FT   3'UTR           852..1643
FT                   /*tag= b
XX
PN   WO200283953-A1.
XX
PD   24-OCT-2002.
XX
```

```
PF   11-APR-2002; 2002WO-US11757.
XX
PR   11-APR-2001; 2001US-282965P.
XX
PA   (PTCT-) PTC THERAPEUTICS INC.
XX
PI   Rando R,  Welch E;
XX
DR   WPI; 2003-075561/07.
XX
PT   Identifying a test compound that binds to a target RNA molecule for
PT   treating or preventing amyloidosis, hemophilia, cancer, gigantism,
PT   diabetes, by contacting a detectably labeled target RNA molecule with a
PT   library of test compounds -
XX
PS   Example; Page 53-54; 152pp; English.
XX
CC   The invention relates to a method for identifying a test compound that
CC   binds to a target RNA molecule, which comprises contacting a detectably
CC   labelled target RNA molecule with a library of test compounds under
CC   conditions that permit direct binding of the labelled target RNA to a
CC   member of the library of test compounds so that a detectably labeled
CC   target RNA:test compound complex is formed. The method is useful for
CC   screening libraries of compounds for those that are selectively bind to
CC   a pre-selected target RNA. The compounds are useful for inhibiting the
CC   formation of a specific bound RNA:host cell factor complexes in vivo.
CC   They are also useful for treating or preventing diseases associated
CC   with overproduction or decreased protein function, such as amyloidosis,
CC   haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism,
CC   dwarfism, hypothyroidism, hyperthyroidism, autoimmune disorders, aging,
CC   inflammation, cystic fibrosis, diabetes, obesity, neurodegenerative
CC   disorders, Parkinson's disease or infections (bacterial, viral, fungal).
CC   The invention is also used in gene therapy. The present sequence is
CC   human tumour necrosis factor alpha (TNF-alpha) DNA. This sequence
CC   is used to illustrate the method of the invention.
XX
SQ   Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 other;

  Query Match             100.0%;  Score 104;  DB 25;  Length 1643;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db       1130 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1173


RESULT 14
AAL53712
ID   AAL53712 standard; DNA; 1643 BP.
XX
AC   AAL53712;
XX
DT   07-FEB-2003  (first entry)
XX
DE   Tumour necrosis factor alpha DNA SEQ ID No 6.
XX
KW   Target RNA; target RNA:support-attached test compound; flow cytometry;
KW   mass spectrometry; high-throughput screening; ds.
XX
OS   Homo sapiens.
XX
PN   WO200283837-A1.
XX
PD   24-OCT-2002.
XX
PF   11-APR-2002; 2002WO-US11758.
XX
PR   11-APR-2001; 2001US-282966P.
XX
PA   (PTCT-) PTC THERAPEUTICS INC.
XX
PI   Almstead NG;
XX
DR   WPI; 2003-075534/07.
XX
PT   Identifying a test compound that binds to a target RNA molecule by
PT   separating the detectably labeled target RNA:support-attached test
PT   compound complex from uncomplexed target RNA molecules and test
PT   compounds by flow cytometry -
XX
PS   Example; Page 44-45; 131pp; English.
XX
CC   The invention relates to a novel method for identifying a test compound
CC   that binds to a target RNA molecule comprising separating the detectably
CC   labeled target RNA:support-attached test compound complex from
CC   uncomplexed target RNA molecules and test compounds. The separating
CC   process is carried out by flow cytometry and determining a structure of
CC   the type of test compound of the RNA:support-attached test compound
CC   complex by mass spectrometry. The method is useful for high-throughput
CC   screening of libraries of compounds to identify pharmaceutical leads.
CC   This polynucleotide sequence represents a DNA sequence related to the
CC   detecting method of the invention.
XX
SQ   Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 other;

  Query Match             100.0%;  Score 104;  DB 25;  Length 1643;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-25;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db       1130 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1173


RESULT 15
AAZ20983
ID   AAZ20983 standard; DNA; 2270 BP.
XX
AC   AAZ20983;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Chimeric nucleic acid -706TNFpGB3'UTR.
XX
KW   TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW   chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW   psoriasis; graft versus host disease; lupus erythematosus;
KW   diabetes; ankylosing spondylitis; rheumatoid arthritis; promoter; ds.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   promoter        7..733
FT                   /*tag=  a
FT                   /label= TNFalpha_promoter
FT                   /note= "Human TNFalpha native promoter (AAZ20973)"
FT   CDS             740..1477
FT                   /*tag=  b
FT                   /product= "Truncated Granzyme B"
FT                   /note= "Inactivating dipeptide absent"
FT   3'UTR           1490..2264
FT                   /*tag=  c
FT                   /label= TNFalpha_3'UTR
XX
PN   WO9943840-A1.
XX
```

PD 02-SEP-1999.
XX
PF 12-JAN-1999; 99WO-US00637.
XX
PR 27-FEB-1998; 98US-0076316.
XX
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Tatake RJ, Marlin SD, Barton RW;
XX
DR WPI; 1999-527630/44.
XX
PT A chimeric polynucleotide consisting of a tumour necrosis factor (TNF)
PT promoter and an apoptosis-inducing Granzyme B polynucleotide -
XX
PS Claim 4; Fig 12; 71pp; English.
XX
CC This sequence represents chimeric nucleic acid -706TNFpGB3'UTR. This
CC comprises at least one TNFalpha (tumour necrosis factor alpha) promoter
CC enhancer region (AAZ20975-Z20978), a TNFalpha native promoter (AAZ20973),
CC a DNA encoding a truncated form of the apoptosis-inducing Granzyme B
CC protein (AAZ20982), and a TNFalpha 3'UTR (untranslated region)
CC sequence (AAZ20979). TNFalpha is one of a number of cytokines
CC produced by inflammatory cells. Upregulation and/or dysregulation
CC of cytokines in inflamed tissue may be directly or indirectly
CC responsible for exacerbation of chronic inflammatory diseases.
CC Introduction of this chimeric nucleotide to activated inflammatory cells
CC causes them to undergo apoptosis. Pharmaceutical compositions of this
CC chimeric nucleotide may be useful for treating inflammatory disorders
CC such as multiple sclerosis, Crohn's disease, ulcerative colitis,
CC psoriasis, graft versus host disease, lupus erythematosus,
CC insulin-dependent (type I) diabetes mellitus, ankylosing spondylitis,
CC and in particular, rheumatoid arthritis. The use of such chimeric
CC nucleotides offers simpler and cheaper long-term relief, in comparison
CC with existing conventional pharmaceutical and invasive surgery methods.
XX
SQ Sequence 2270 BP; 556 A; 647 C; 545 G; 522 T; 0 other;

Query Match 100.0%; Score 104; DB 20; Length 2270;
Best Local Similarity 100.0%; Pred. No. 3.1e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1705 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1764

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1765 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1808
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Job time : 290.946 secs

GenCore version 5.1.6

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Perfect score: 104
Sequence: 1 gaattcaaactggggcctcc.....ggttctggccagaatgctgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	104	100.0	787	4	US-09-032-297A-13	Sequence 13, Appl
	2	104	100.0	787	4	US-09-229-151C-7	Sequence 7, Appli
	3	104	100.0	1643	3	US-08-880-342-36	Sequence 36, Appl
	4	104	100.0	1643	4	US-09-505-250-4	Sequence 4, Appli
	5	104	100.0	2270	4	US-09-229-151C-13	Sequence 13, Appl
	6	104	100.0	2570	4	US-09-229-151C-14	Sequence 14, Appl
	7	104	100.0	3634	3	US-09-166-186-1	Sequence 1, Appli
	8	104	100.0	3634	3	US-09-313-932-1	Sequence 1, Appli
	9	104	100.0	3634	3	US-09-109-663-34	Sequence 34, Appl
c	10	28	26.9	28720	4	US-09-341-587-7	Sequence 7, Appli
	11	27.4	26.3	116592	4	US-09-818-512-3	Sequence 3, Appli
	12	26.4	25.4	3170	4	US-09-169-768-1	Sequence 1, Appli
	13	26.4	25.4	3171	4	US-09-169-768-15	Sequence 15, Appl
	14	26.4	25.4	3181	1	US-08-655-086-1	Sequence 1, Appli
	15	26.4	25.4	3349	4	US-09-169-768-13	Sequence 13, Appl
	16	26.4	25.4	3531	4	US-09-169-768-7	Sequence 7, Appli
	17	26.4	25.4	3541	4	US-09-169-768-9	Sequence 9, Appli
c	18	25.8	24.8	3889	4	US-09-484-970B-39	Sequence 39, Appl
	19	25.8	24.8	4031	1	US-08-159-784-1	Sequence 1, Appli
c	20	25.6	24.6	642	3	US-09-328-111-82	Sequence 82, Appl
c	21	25.6	24.6	1923	4	US-09-620-312D-1004	Sequence 1004, Ap
c	22	25.6	24.6	2634	3	US-08-911-853-30	Sequence 30, Appl
c	23	25.6	24.6	2634	3	US-09-479-409-30	Sequence 30, Appl
c	24	25.6	24.6	2634	4	US-09-479-453-30	Sequence 30, Appl
c	25	25.6	24.6	17612	3	US-08-911-853-29	Sequence 29, Appl
c	26	25.6	24.6	17612	3	US-09-479-409-29	Sequence 29, Appl
c	27	25.6	24.6	17612	4	US-09-479-453-29	Sequence 29, Appl
	28	25.4	24.4	220	3	US-09-263-933-22	Sequence 22, Appl
	29	25.4	24.4	604	3	US-09-068-880-1	Sequence 1, Appli
	30	25.4	24.4	1026	3	US-09-068-880-14	Sequence 14, Appl
	31	25.4	24.4	1289	4	US-09-247-155-138	Sequence 138, App
	32	25.4	24.4	1467	3	US-09-330-317B-17	Sequence 17, Appl
	33	25.4	24.4	1467	4	US-09-808-589A-17	Sequence 17, Appl
	34	25.4	24.4	1956	3	US-08-867-352-20	Sequence 20, Appl
	35	25.4	24.4	4145	1	US-08-314-917-1	Sequence 1, Appli
	36	25.4	24.4	4145	1	US-08-265-046-1	Sequence 1, Appli
	37	25.4	24.4	4145	2	US-08-465-522-1	Sequence 1, Appli
	38	25.4	24.4	4145	5	PCT-US93-11401-1	Sequence 1, Appli
	39	25.4	24.4	4145	5	PCT-US95-07849-1	Sequence 1, Appli
	40	25.4	24.4	4951	2	US-08-752-307B-1	Sequence 1, Appli
	41	25.4	24.4	4951	4	US-09-707-802-1	Sequence 1, Appli
	42	25.4	24.4	4951	4	US-09-991-326-1	Sequence 1, Appli
	43	25.4	24.4	7076	4	US-09-837-863-20	Sequence 20, Appl
	44	25.4	24.4	7076	4	US-09-837-863-21	Sequence 21, Appl
	45	25.4	24.4	7092	4	US-09-837-863-19	Sequence 19, Appl

ALIGNMENTS

```
RESULT 1
US-09-032-297A-13
; Sequence 13, Application US/09032297A
; Patent No. 6525184
;  GENERAL INFORMATION:
;       APPLICANT: Revati J. Tatake, Steven D. Marlin and
;                  Randall W. Barton
;       TITLE OF INVENTION: Self-Regulated Apoptosis of
;                           Inflammatory Cells by Gene Therapy
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Boehringer Ingelheim Corporation
;            STREET: 900 Ridgebury Road, P.O. Box 368
;            CITY: Ridgefield
;            STATE: Connecticut
;            COUNTRY: United States of America
;            ZIP: 06877-0368
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5" 1.44 Mb diskette
;            COMPUTER: IBM PC
;            OPERATING SYSTEM: MS DOS
;            SOFTWARE: Word Processing
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/032,297A
;            FILING DATE: 27-Feb-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/038,266
;            FILING DATE: 28-FEB-97
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Robert P. Raymond
;            REGISTRATION NUMBER: 25089
;            REFERENCE/DOCKET NUMBER: 9/121PCT
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 203-791-6183
;  INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 787
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: <Unknown>
;            DESCRIPTION: DNA
;       FEATURE:
;            NAME/KEY:  TNFa 3' untranslated region
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-032-297A-13

  Query Match           100.0%;  Score 104;  DB 4;  Length 787;
  Best Local Similarity  100.0%;  Pred. No. 5.7e-27;
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  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 281

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 325


RESULT 2
US-09-229-151C-7
; Sequence 7, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
;  APPLICANT: Tatake, Revati J.
;  APPLICANT:  Marlin, Steven D.
;  APPLICANT:  Barton, Randall W.
;  TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
;  FILE REFERENCE: 9/137
;  CURRENT APPLICATION NUMBER: US/09/229,151C
;  CURRENT FILING DATE:  1999-01-12
;  PRIOR APPLICATION NUMBER: US 60/076,316
;  PRIOR FILING DATE: 1998-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 2.0
; SEQ ID NO 7
;   LENGTH: 787
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   OTHER INFORMATION: TNF-alpha untranslated region
US-09-229-151C-7

  Query Match            100.0%;  Score 104;  DB 4;  Length 787;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 281

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db        282 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 325


RESULT 3
US-08-880-342-36
; Sequence 36, Application US/08880342
; Patent No. 6218179
;  GENERAL INFORMATION:
;    APPLICANT:  Webster, Keith A.
;    APPLICANT:  Bishopric, Nanette H.
;    APPLICANT:  Murphy, Brian
;    APPLICANT:  Laderoute, Keith R.
;    APPLICANT:  Green, Christopher J.
;    TITLE OF INVENTION:  Tissue Specific Hypoxia Regulated
;    TITLE OF INVENTION:  Therapeutic Constructs
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Avenue, Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/880,342
;      FILING DATE:  23-JUN-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB95/00996
;      FILING DATE:  13-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/365,486
;      FILING DATE:  23-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sholtz, Charles K.
;      REGISTRATION NUMBER:  38,615
;      REFERENCE/DOCKET NUMBER:  8255-0018.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 324-0880
;      TELEFAX:  (415) 324-0960
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1643 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      INDIVIDUAL ISOLATE:  TNF cDNA HSTNFR (EMBL Accession
;      INDIVIDUAL ISOLATE:  #X01394)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  153..851
US-08-880-342-36

  Query Match            100.0%;  Score 104;  DB 3;  Length 1643;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1130 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1173


RESULT 4
US-09-505-250-4
; Sequence 4, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
;  APPLICANT:  Rosen, Glenn
;  APPLICANT:  Kao, Peter
;  TITLE OF INVENTION:  Synergistic Anti-Cancer Therapy with
;  TITLE OF INVENTION:  Triptolides and Death Domain Ligands
;  FILE REFERENCE:  SUN-109PRV2
;  CURRENT APPLICATION NUMBER: US/09/505,250A
;  CURRENT FILING DATE:  2000-02-15
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 1643
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (153)...(854)
US-09-505-250-4

  Query Match            100.0%;  Score 104;  DB 4;  Length 1643;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1130 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1173


RESULT 5
US-09-229-151C-13
; Sequence 13, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
;  APPLICANT: Tatake, Revati J.
;  APPLICANT:  Marlin, Steven D.
;  APPLICANT:  Barton, Randall W.
;  TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
;  FILE REFERENCE: 9/137
;  CURRENT APPLICATION NUMBER: US/09/229,151C
;  CURRENT FILING DATE:  1999-01-12
;  PRIOR APPLICATION NUMBER: US 60/076,316
;  PRIOR FILING DATE: 1998-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 2.0
; SEQ ID NO 13
;   LENGTH: 2270
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   OTHER INFORMATION: chimeric gene : -706TNFpGB3'UTR
US-09-229-151C-13

  Query Match             100.0%;  Score 104;  DB 4;  Length 2270;
  Best Local Similarity   100.0%;  Pred. No. 8e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1705 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1764

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1765 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1808


RESULT 6
US-09-229-151C-14
; Sequence 14, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
;  APPLICANT: Tatake, Revati J.
;  APPLICANT:  Marlin, Steven D.
;  APPLICANT:  Barton, Randall W.
;  TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
;  FILE REFERENCE: 9/137
;  CURRENT APPLICATION NUMBER: US/09/229,151C
;  CURRENT FILING DATE:  1999-01-12
;  PRIOR APPLICATION NUMBER: US 60/076,316
;  PRIOR FILING DATE: 1998-02-27
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 2.0
; SEQ ID NO 14
;   LENGTH: 2570
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   OTHER INFORMATION: chimeric gene : -1005TNFpGB3'UTR
US-09-229-151C-14

  Query Match             100.0%;  Score 104;  DB 4;  Length 2570;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2005 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2064

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db       2065 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 2108


RESULT 7
US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda
;  APPLICANT: Bennett, C. Frank
;  APPLICANT: Butler, Madeline M.
;  APPLICANT: Shanahan, William R.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
;  FILE REFERENCE: ISPH-0322
;  CURRENT APPLICATION NUMBER: US/09/166,186A
;  CURRENT FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 1
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (615)..(981)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (982)..(1588)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1589)..(1634)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (1635)..(1821)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1822)..(1869)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (1870)..(2070)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (2171)..(3381)
;   PUBLICATION INFORMATION:
;   AUTHORS: Nedwin, G.E.
;   AUTHORS: Naylor, S.L.
;   AUTHORS: Sakaguchi, A.Y.
;   AUTHORS: Smith, D.
;   AUTHORS: Jarrett-Nedwin, J.
;   AUTHORS: Pennica, D.
;   AUTHORS: Goeddel, D.V.
;   AUTHORS: Gray, P.W.
;   TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,
;   TITLE: homology and chromosomal localization
;   JOURNAL: Nucleic Acids Res.
;   VOLUME: 13
;   ISSUE: 17
;   PAGES: 6361-6373
;   DATE: 1985-09-11
;   DATABASE ACCESSION NUMBER: X02910 Genbank
;   DATABASE ENTRY DATE: 1997-02-17
US-09-166-186-1
```

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  Query Match           100.0%;  Score 104;  DB 3;  Length 3634;
  Best Local Similarity  100.0%;  Pred. No. 9.2e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db       2868 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 2911


RESULT 8
US-09-313-932-1
; Sequence 1, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda
;  APPLICANT: Bennett, C. Frank
;  APPLICANT: Butler, Madeline M.
;  APPLICANT: Shanahan, William R.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
;  TITLE OF INVENTION: EXPRESSION
;  FILE REFERENCE: ISPH-0356
;  CURRENT APPLICATION NUMBER: US/09/313,932A
;  CURRENT FILING DATE: 1999-05-18
;  NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 1
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (615)..(981)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (982)..(1588)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1589)..(1634)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (1635)..(1821)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1822)..(1869)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (1870)..(2070)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (2171)..(3381)
;  PUBLICATION INFORMATION:
;   AUTHORS: Nedwin, G.E.
;   AUTHORS: Naylor, S.L.
;   AUTHORS: Sakaguchi, A.Y.
;   AUTHORS: Smith, D.
;   AUTHORS: Jarrett-Nedwin, J.
;   AUTHORS: Pennica, D.
;   AUTHORS: Goeddel, D.V.
;   AUTHORS: Gray, P.W.
;   TITLE: Human lymphotoxin and tumor necrosis factor genes:
;   TITLE: structure, homology and chromosomal localization
;   JOURNAL: Nucleic Acids Res.
;   VOLUME: 13
;   ISSUE: 17
;   PAGES: 6361-6373
;   DATE: 1985-09-11
;   DATABASE ACCESSION NUMBER: X02910 Genbank
;   DATABASE ENTRY DATE: 1997-02-17
US-09-313-932-1

  Query Match           100.0%;  Score 104;  DB 3;  Length 3634;
  Best Local Similarity  100.0%;  Pred. No. 9.2e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db       2868 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 2911


RESULT 9
US-09-109-663-34
; Sequence 34, Application US/09109663
; Patent No. 6277981
; GENERAL INFORMATION:
;  APPLICANT: Tu, Guang-Chou
;  APPLICANT: Israel, Yedy
;  TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
;  TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
;  FILE REFERENCE: 9855-3U1
;  CURRENT APPLICATION NUMBER: US/09/109,663
;  CURRENT FILING DATE: 1998-07-03
;  EARLIER APPLICATION NUMBER: 60/051,705
;  EARLIER FILING DATE: 1997-07-03
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: TNF(alpha) cDNA
US-09-109-663-34

  Query Match           100.0%;  Score 104;  DB 3;  Length 3634;
  Best Local Similarity  100.0%;  Pred. No. 9.2e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||
Db       2868 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 2911


RESULT 10
US-09-341-587-7/c
; Sequence 7, Application US/09341587
; Patent No. 6346606
; GENERAL INFORMATION:
;  APPLICANT: Mollenhauer, Jan
;  TITLE OF INVENTION: Protein Containing an SRCR Domain
;  FILE REFERENCE: 4121-108
;  CURRENT APPLICATION NUMBER: US/09/341,587
;  CURRENT FILING DATE: 1999-08-31
;  EARLIER APPLICATION NUMBER: PCT/DE98/00096
;  EARLIER FILING DATE: 1998-01-09
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 28720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-341-587-7
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  Query Match           26.9%;  Score 28;  DB 4;  Length 28720;
  Best Local Similarity  58.3%;  Pred. No. 4.3;
  Matches   49;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          2 AATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGG 61
              ||||  ||  ||| |||  |||     |  |||| |  |  | |||  ||  | | || ||
Db      14762 AATTTGAAGAGGGTCCTAGAGAGGAGAGAGGGGACATCTCCATTGTACCAGGTCTTCAGG 14703

Qy         62 AATCTGGAGACCAGGGAGCCTTTG 85
              || | | ||| ||| | | | ||
Db      14702 TATTTTGTGACAAGGAATCATCTG 14679


RESULT 11
US-09-818-512-3
; Sequence 3, Application US/09818512
; Patent No. 6537780
; GENERAL INFORMATION:
;  APPLICANT: BEASLEY, Ellen et al.
;  TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001192
;  CURRENT APPLICATION NUMBER: US/09/818,512
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 116592
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(116592)
;   OTHER INFORMATION: n = A,T,C or G
US-09-818-512-3

  Query Match           26.3%;  Score 27.4;  DB 4;  Length 116592;
  Best Local Similarity  54.5%;  Pred. No. 11;
  Matches   55;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          4 TTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGAA 63
              | ||||||   |||   ||   ||  |    ||  ||  ||| | ||| || || |  |
Db      81506 TCCAAACTATTGCCAGTAGCTTTCTGTTTTCCCATCATTTTTCAACCCAGAAATATTTAT 81565

Qy         64 TCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              | |      |||||||| | || |   |  || | ||| |
Db      81566 TTTTCTTTCCAGGGAGGCATTAGCAGTACCCTGGAAGCTCC 81606


RESULT 12
US-09-169-768-1
; Sequence 1, Application US/09169768
; Patent No. 6492508
;  GENERAL INFORMATION:
;    APPLICANT:  GRUSKIN, ELLIOT A.
;    APPLICANT:  BUECHTER, DOUGLAS
;    APPLICANT:  BROKAW, JANE
;    APPLICANT:  ZHANG, GUANGHUI
;    APPLICANT:  PAOLELLA, DAVID
;    TITLE OF INVENTION:  AMINO ACID MODIFIED POLYPEPTIDES
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DILWORTH & BARRESE
;      STREET:  333 EARLE OVINGTON BOULEVARD
;      CITY:  UNIONDALE
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  11553
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/169,768
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEEN, JEFFREY S
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 228-8484
;      TELEFAX:  (516) 228-8516
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3170 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-169-768-1

  Query Match           25.4%;  Score 26.4;  DB 4;  Length 3170;
  Best Local Similarity  57.1%;  Pred. No. 7.7;
  Matches   48;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          8 AACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGAATCTG 67
              | |  ||   ||| | || | |||| ||  | |   || | |  | ||   ||  |||
Db       1307 AGCGAGGTGTTCCCGGACCCCCTGGCGCTGTCGGTCCTGCTGGCAAAGATGGAGAGGCTG 1366

Qy         68 GAGACCAGGGAGCCTTTGGTTCTG 91
              |||  |||||| ||  |||  |||
Db       1367 GAGCTCAGGGACCCCCTGGCCCTG 1390


RESULT 13
US-09-169-768-15
; Sequence 15, Application US/09169768
; Patent No. 6492508
;  GENERAL INFORMATION:
;    APPLICANT:  GRUSKIN, ELLIOT A.
;    APPLICANT:  BUECHTER, DOUGLAS
;    APPLICANT:  BROKAW, JANE
;    APPLICANT:  ZHANG, GUANGHUI
;    APPLICANT:  PAOLELLA, DAVID
;    TITLE OF INVENTION:  AMINO ACID MODIFIED POLYPEPTIDES
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DILWORTH & BARRESE
;      STREET:  333 EARLE OVINGTON BOULEVARD
;      CITY:  UNIONDALE
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  11553
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/169,768
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEEN, JEFFREY S
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 228-8484
;      TELEFAX:  (516) 228-8516
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3171 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-169-768-15
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  Query Match           25.4%;  Score 26.4;  DB 4;  Length 3171;
  Best Local Similarity  57.1%;  Pred. No. 7.7;
  Matches   48;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

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Qy         68 GAGACCAGGGAGCCTTTGGTTCTG 91
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RESULT 14
US-08-655-086-1
; Sequence 1, Application US/08655086
; Patent No. 5821089
;  GENERAL INFORMATION:
;    APPLICANT:  GRUSKIN, ELLIOTT A.
;    APPLICANT:  BUECHTER, DOUGLAS
;    APPLICANT:  ZHANG, GUANGHUI
;    APPLICANT:  CONNOLLY, KEVIN
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DILWORTH & BARRESE
;      STREET:  333 EARLE OVINGTON BOULEVARD
;      CITY:  UNIONDALE
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  11553
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/655,086
;      FILING DATE:  03-JUN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEEN, JEFFREY S.
;      REGISTRATION NUMBER:  32,063
;      REFERENCE/DOCKET NUMBER:  203-1632
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  516-228-8484
;      TELEFAX:  516-228-8516
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3181 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
US-08-655-086-1

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  Matches   48;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

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Qy         68 GAGACCAGGGAGCCTTTGGTTCTG 91
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Db       1377 GAGCTCAGGGACCCCCTGGCCCTG 1400


RESULT 15
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; Sequence 13, Application US/09169768
; Patent No. 6492508
;  GENERAL INFORMATION:
;    APPLICANT:  GRUSKIN, ELLIOT A.
;    APPLICANT:  BUECHTER, DOUGLAS
;    APPLICANT:  BROKAW, JANE
;    APPLICANT:  ZHANG, GUANGHUI
;    APPLICANT:  PAOLELLA, DAVID
;    TITLE OF INVENTION:  AMINO ACID MODIFIED POLYPEPTIDES
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DILWORTH & BARRESE
;      STREET:  333 EARLE OVINGTON BOULEVARD
;      CITY:  UNIONDALE
;      STATE:  NY
;      COUNTRY:  U.S.A.
;      ZIP:  11553
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/169,768
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEEN, JEFFREY S
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (516) 228-8484
;      TELEFAX:  (516) 228-8516
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3349 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-169-768-13

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  Best Local Similarity  57.1%;  Pred. No. 7.9;
  Matches   48;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

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Qy         68 GAGACCAGGGAGCCTTTGGTTCTG 91
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Job time : 85.6531 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 3, 2004, 05:14:03 ; Search time 1850.07 Seconds
(without alignments)
207.072 Million cell updates/sec

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Perfect score: 104
Sequence: 1 gaattcaaactggggcctcc.....ggttctggccagaatgctgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	104	100.0	104	10	US-09-801-371A-1	Sequence 1, Appli
c	2	104	100.0	104	10	US-09-801-371A-5	Sequence 5, Appli
	3	104	100.0	1643	13	US-10-310-793-9	Sequence 9, Appli
	4	104	100.0	1643	15	US-10-272-411-4	Sequence 4, Appli
	5	104	100.0	1643	15	US-10-218-547-3	Sequence 3, Appli
	6	104	100.0	1643	15	US-10-272-328A-4	Sequence 4, Appli
	7	104	100.0	1666	13	US-10-247-671-68	Sequence 68, Appl
	8	104	100.0	3634	11	US-09-824-322B-1	Sequence 1, Appli
	9	104	100.0	3634	11	US-09-932-300-34	Sequence 34, Appl
	10	104	100.0	3634	13	US-10-191-997-104	Sequence 104, App
	11	104	100.0	4830	12	US-10-429-802-33	Sequence 33, Appl
	12	104	100.0	4830	12	US-10-430-503-24	Sequence 24, Appl
	13	93	89.4	1279	13	US-10-247-671-120	Sequence 120, App
	14	77	74.0	81	10	US-09-801-371A-7	Sequence 7, Appli
	15	59.8	57.5	3673778	13	US-10-312-841-1	Sequence 1, Appli
c	16	58.2	56.0	3673778	13	US-10-312-841-2	Sequence 2, Appli
	17	50	48.1	50	10	US-09-801-371A-8	Sequence 8, Appli
	18	43	41.3	43	10	US-09-801-371A-2	Sequence 2, Appli
c	19	43	41.3	43	10	US-09-801-371A-6	Sequence 6, Appli
	20	42	40.4	418	10	US-09-796-692-6223	Sequence 6223, Ap
	21	42	40.4	418	12	US-10-057-475B-6223	Sequence 6223, Ap
	22	42	40.4	418	12	US-10-154-884B-6223	Sequence 6223, Ap
	23	42	40.4	418	15	US-10-040-862-6223	Sequence 6223, Ap
	24	33	31.7	51	10	US-09-801-371A-10	Sequence 10, Appl
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	26	30.4	29.2	440	12	US-10-062-674-37	Sequence 37, Appl
	27	30.2	29.0	45855	12	US-10-085-117-316	Sequence 316, App
c	28	29.2	28.1	2643	12	US-10-108-260A-754	Sequence 754, App
c	29	28.8	27.7	1223197	13	US-10-027-632-179264	Sequence 179264,
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c	31	27.6	26.5	232	12	US-10-242-535A-46829	Sequence 46829, A
c	32	27.4	26.3	3617	9	US-09-874-069-2	Sequence 2, Appli
	33	27.4	26.3	116592	10	US-09-818-512-3	Sequence 3, Appli
	34	27.4	26.3	116592	13	US-10-354-065-3	Sequence 3, Appli
c	35	27.2	26.2	494	13	US-10-027-632-280709	Sequence 280709,
c	36	27.2	26.2	494	14	US-10-027-632-280709	Sequence 280709,
c	37	27.2	26.2	1392	15	US-10-156-761-524	Sequence 524, App
	38	27.2	26.2	45000	15	US-10-000-213-12	Sequence 12, Appl
	39	27.2	26.2	122186	11	US-09-563-728A-36	Sequence 36, Appl
c	40	27.2	26.2	9025608	15	US-10-156-761-1	Sequence 1, Appli
c	41	27	26.0	860	13	US-10-027-632-8841	Sequence 8841, Ap
c	42	27	26.0	860	14	US-10-027-632-8841	Sequence 8841, Ap
	43	27	26.0	2895	12	US-10-159-563-71	Sequence 71, Appl
	44	27	26.0	2895	13	US-10-133-937-71	Sequence 71, Appl
	45	27	26.0	2915	13	US-10-354-358-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-801-371A-1
; Sequence 1, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-1

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Best Local Similarity 100.0%; Pred. No. 6.3e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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US-09-801-371A-5/c
; Sequence 5, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
;  APPLICANT: Kaempfer, Raymond
;  APPLICANT:  Osman, Farhat
;  APPLICANT:  Jarrous, Nayef
;  APPLICANT:  Ben-Asouli, Yitzhak
;  TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
;  TITLE OF INVENTION:  MANIPULATION OF MRNA SPLICING AND ITS USES
;  FILE REFERENCE: A34084-PCT-USA-A 066031.0147
;  CURRENT APPLICATION NUMBER: US/09/801,371A
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: PCT WO 00/14255
;  PRIOR FILING DATE: 1999-09-06
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 104
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-801-371A-5

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  Best Local Similarity  100.0%;  Pred. No. 6.3e-28;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-10-310-793-9
; Sequence 9, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
;  APPLICANT: Yu, Guo-Liang
;  APPLICANT:  Ni, Jian
;  APPLICANT:  Rosen, Craig A
;  APPLICANT:  Zhang, Jun
;  APPLICANT:  Wei, Ping
;  TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
;  TITLE OF INVENTION:  Relating To Human Tumor Necrosis Factor-Gamma Beta
;  FILE REFERENCE: PF573
;  CURRENT APPLICATION NUMBER: US/10/310,793
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: 60/336,695
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: 10/226,294
;  PRIOR FILING DATE: 2002-08-23
;  PRIOR APPLICATION NUMBER: 60/314,381
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: 09/899,059
;  PRIOR FILING DATE: 2001-07-06
;  PRIOR APPLICATION NUMBER: 60/278,449
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: 60/216,879
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: 09/559,290
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 60/180,908
;  PRIOR FILING DATE: 2000-02-08
;  PRIOR APPLICATION NUMBER: 60/134,067
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/132,227
;  PRIOR FILING DATE: 1999-05-03
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 1643
;   TYPE: DNA
;   ORGANISM: human
US-10-310-793-9

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  Best Local Similarity  100.0%;  Pred. No. 1e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 4
US-10-272-411-4
; Sequence 4, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
;  APPLICANT: Barnes Jewish Hospital
;  APPLICANT:  Lam, Jonathan
;  APPLICANT:  Ross, F. Patrick
;  APPLICANT:  Teitelbaum, Steven
;  TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
;  FILE REFERENCE: 60019620-0202
;  CURRENT APPLICATION NUMBER: US/10/272,411
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/329,393
;  PRIOR FILING DATE: 2001-10-15
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1643
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/ X01394.1
;   DATABASE ENTRY DATE: 1995-03-21
;   RELEVANT RESIDUES: (1)..(1643)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
;   DATABASE ENTRY DATE: 2002-05-01
;   RELEVANT RESIDUES: (1)..(1643)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/ M35592.1
;   DATABASE ENTRY DATE: 1993-04-27
;   RELEVANT RESIDUES: (1)..(1643)
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
;   DATABASE ENTRY DATE: 2002-08-01
;   RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4

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  Best Local Similarity  100.0%;  Pred. No. 1e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 3, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
;  TITLE OF INVENTION:  Human Endokine Alpha
;  FILE REFERENCE: PF561
;  CURRENT APPLICATION NUMBER: US/10/218,547
;  CURRENT FILING DATE:  2002-08-15
;  PRIOR APPLICATION NUMBER: 60/312,542
;  PRIOR FILING DATE: 2001-08-16
;  PRIOR APPLICATION NUMBER: 60/330,761
;  PRIOR FILING DATE: 2001-10-30
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 1643
;   TYPE: DNA
;   ORGANISM: human
US-10-218-547-3

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  Best Local Similarity   100.0%;  Pred. No. 1e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 6
US-10-272-328A-4
; Sequence 4, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
;  APPLICANT: Barnes Jewish Hospital
;  APPLICANT:  Lam, Jonathan
;  APPLICANT:  Ross, F. Patrick
;  APPLICANT:  Teitelbaum, Steven
;  TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
;  FILE REFERENCE: 60019620-0206
;  CURRENT APPLICATION NUMBER: US/10/272,328A
;  CURRENT FILING DATE:  2003-01-24
;  PRIOR APPLICATION NUMBER: 60/329,393
;  PRIOR FILING DATE: 2001-10-15
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 1643
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-272-328A-4

  Query Match             100.0%;  Score 104;  DB 15;  Length 1643;
  Best Local Similarity   100.0%;  Pred. No. 1e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1130 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1173


RESULT 7
US-10-247-671-68
; Sequence 68, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
;  APPLICANT: Mikita, Thomas
;  APPLICANT:  Shiffman, Dov
;  APPLICANT:  Porter, Gordon, J.
;  APPLICANT:  Kaser, Matthew R.
;  TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
;  FILE REFERENCE: PA-0050 US
;  CURRENT APPLICATION NUMBER: US/10/247,671
;  CURRENT FILING DATE:  2002-09-18
;  PRIOR APPLICATION NUMBER: 60/323,784
;  PRIOR FILING DATE: 2001-09-19
;  NUMBER OF SEQ ID NOS: 186
;  SOFTWARE: PERL Program
; SEQ ID NO 68
;   LENGTH: 1666
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030194721A1 223092.1
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 1347, 1358
;   OTHER INFORMATION: a, t, c, g, or other
US-10-247-671-68

  Query Match             100.0%;  Score 104;  DB 13;  Length 1666;
  Best Local Similarity   100.0%;  Pred. No. 1e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1085 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1144

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1145 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1188


RESULT 8
US-09-824-322B-1
; Sequence 1, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Brenda
;  APPLICANT:  Bennett, C. Frank
;  APPLICANT:  Butler, Madeline M.
;  APPLICANT:  Shanahan, William R.
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-AL
;  TITLE OF INVENTION:  ALPHA) EXPRESSION
;  FILE REFERENCE: ISPH-0501
;  CURRENT APPLICATION NUMBER: US/09/824,322B
;  CURRENT FILING DATE:  2001-04-02
;  PRIOR APPLICATION NUMBER: US 09/313,932
;  PRIOR FILING DATE: 1999-05-18
;  PRIOR APPLICATION NUMBER: US 09/166,186
;  PRIOR FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 1
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
;   NAME/KEY: exon
;   LOCATION: (615)..(981)
;   NAME/KEY: intron
;   LOCATION: (982)..(1588)
;   NAME/KEY: exon
;   LOCATION: (1589)..(1634)
```

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;   NAME/KEY: intron
;   LOCATION: (1635)..(1821)
;   NAME/KEY: exon
;   LOCATION: (1822)..(1869)
;   NAME/KEY: intron
;   LOCATION: (1870)..(2070)
;   NAME/KEY: exon
;   LOCATION: (2171)..(3381)
;  PUBLICATION INFORMATION:
;   AUTHORS: Nedwin, G.E.
;   AUTHORS: Naylor, S.L.
;   AUTHORS: Sakaguchi, A.Y.
;   AUTHORS: Smith, D.
;   AUTHORS: Jarrett-Nedwin, J.
;   AUTHORS: Pennica, D.
;   AUTHORS: Goeddel, D.V.
;   AUTHORS: Gray, P.W.
;   TITLE: Human lymphotoxin and tumor necrosis factor genes: structure, homology and
;   TITLE: chromosomal localization
;   JOURNAL: Nucleic Acids Res.
;   VOLUME: 13
;   ISSUE: 17
;   PAGES: 6361-6373
;   DATE: 1985-09-11
;   DATABASE ACCESSION NUMBER: X02910 Genbank
;   DATABASE ENTRY DATE: 1997-02-17
US-09-824-322B-1

  Query Match            100.0%;  Score 104;  DB 11;  Length 3634;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db       2868 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 2911


RESULT 9
US-09-932-300-34
; Sequence 34, Application US/09932300
; Publication No. US20030032788A1
; GENERAL INFORMATION:
;  APPLICANT: GARVER, Eric
;  APPLICANT:  TU, Guang-Chou
;  APPLICANT:  ISRAEL, Yedy
;  TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION
;  FILE REFERENCE: 9855-3U2
;  CURRENT APPLICATION NUMBER: US/09/932,300
;  CURRENT FILING DATE:  2001-08-20
;  PRIOR APPLICATION NUMBER: US 60/051,705
;  PRIOR FILING DATE: 1997-07-03
;  PRIOR APPLICATION NUMBER: US 09/109,663
;  PRIOR FILING DATE: 1998-07-02
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-932-300-34

  Query Match            100.0%;  Score 104;  DB 11;  Length 3634;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db       2868 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 2911


RESULT 10
US-10-191-997-104
; Sequence 104, Application US/10191997
; Publication No. US20030207834A1
; GENERAL INFORMATION:
;  APPLICANT: Oligos Etc., Inc.
;  APPLICANT:  DALE, Roderic M. K.
;  APPLICANT:  ARROW, Amy
;  APPLICANT:  THOMPSON, Terry
;  TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Thei
;  FILE REFERENCE: 54800-5019
;  CURRENT APPLICATION NUMBER: US/10/191,997
;  CURRENT FILING DATE:  2002-07-10
;  PRIOR APPLICATION NUMBER: US 60/303,820
;  PRIOR FILING DATE: 2001-07-10
;  NUMBER OF SEQ ID NOS: 132
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
;   LENGTH: 3634
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: X02910
US-10-191-997-104

  Query Match            100.0%;  Score 104;  DB 13;  Length 3634;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db       2868 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 2911


RESULT 11
US-10-429-802-33
; Sequence 33, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:
;  APPLICANT: HUNG, MIEN-CHIE
;  APPLICANT:  WONG, KA YIN
;  APPLICANT:  ZOU, YIYU
;  TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
;  FILE REFERENCE: UTSC:752US
;  CURRENT APPLICATION NUMBER: US/10/429,802
;  CURRENT FILING DATE:  2003-05-05
;  PRIOR APPLICATION NUMBER: 60/377,672
;  PRIOR FILING DATE: 2002-05-03
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
;   LENGTH: 4830
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-429-802-33

  Query Match            100.0%;  Score 104;  DB 12;  Length 4830;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-27;
  Matches  104;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2781 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2840
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```
Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db       2841 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 2884
```

RESULT 12
US-10-430-503-24
; Sequence 24, Application US/10430503
; Publication No. US20040005684A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LAN, KENG-LI
; APPLICANT: OU-YANG, FU
; APPLICANT: LIU, JAW-CHING
; APPLICANT: LAN, KENG-HSIN
; TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
; TITLE OF INVENTION: REAGENTS
; FILE REFERENCE: UTSC:797US
; CURRENT APPLICATION NUMBER: US/10/430,503
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/383,063
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 4830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-430-503-24

Query Match 100.0%; Score 104; DB 12; Length 4830;
Best Local Similarity 100.0%; Pred. No. 1.2e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2781 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2840

Qy         61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||||||||||||||||||||||||||||||||
Db       2841 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 2884
```

RESULT 13
US-10-247-671-120
; Sequence 120, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 120
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 561301CB1
US-10-247-671-120

Query Match 89.4%; Score 93; DB 13; Length 1279;
Best Local Similarity 99.0%; Pred. No. 9.5e-24;
Matches 104; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1077 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1136

Qy         61 GAATCTGGAGACCA-GGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
              ||||||||||||||| ||||||||||||||||||||||||||||
Db       1137 GAATCTGGAGACCAGGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1181
```

RESULT 14
US-09-801-371A-7
; Sequence 7, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 81
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-7

Query Match 74.0%; Score 77; DB 10; Length 81;
Best Local Similarity 79.2%; Pred. No. 3.8e-18;
Matches 61; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
              |||::|||||:||||||:|||||||:|||:|||||||:|||||:::||:|||:||||:|:|
Db          5 GAAUUCAAACUGGGGCCUCCAGAACUCACUGGGGCCUACAGCUUUGAUCCCUGACAUCUG 64

Qy         61 GAATCTGGAGACCAGGG 77
              |||:|:|||||||||||
Db         65 GAAUCUGGAGACCAGGG 81
```

RESULT 15
US-10-312-841-1
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MH
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Query Match 57.5%; Score 59.8; DB 13; Length 3673778;
Best Local Similarity 73.8%; Pred. No. 4.1e-11;
Matches 76; Conservative 0; Mismatches 27; Indels 0; Gaps 0;